

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2003, 19:38:05 : Search time 299 Seconds
(without alignments)
1852.815 Million cell updates/sec

Title: US-10-036-041-2
Perfect score: 1367
Sequence: 1 MLMROLIYQMLAFLFLPC.....LHGHDQRFSTFAGFLLETK 246

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 218539 segs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL-frame+ -p2n.model -DEV=xlp
-Q/cg2.1/USPTO.spool/US10036041/runal_13012003_160808_7048/app-query.fasta.1.391
-DB=N.Geneseq.101002 -OPMT=fastlap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=ptc -NORM=ext -HRAPIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10036041.ecgn.1.1.79_etunal_13012003_160808_7048 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.Geneseq.101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1367	100.0	741	ABK35591	Gene encoding nove
2	1367	100.0	1696	ABK44058	Human zacr3p3 CDNA,
3	1367	100.0	1709	AAK3874	Human CDNA encodin
4	1367	100.0	1712	AAA96336	CDNA encoding a no
5	1367	100.0	1760	AAA95787	Human immune syste
6	1320.5	96.6	960	ABK35590	Gene encoding nove
7	1311	95.9	1035	AAK99776	Skin cell CDNA, SE
8	1311	95.9	1035	ABK34928	Rat CDNA isolated
9	1311	95.9	1117	AAK64064	Mouse zacr2p2 DNA,
10	1311	95.9	1123	AAK61633	CDNA encoding rat
11	1311	95.9	1123	AAK61730	CDNA encoding rat
12	1311	95.9	1123	AAK99566	Skin cell CDNA, SE
13	1311	95.9	1123	AAK99663	Skin cell CDNA, SE
14	1311	95.9	1123	ABK34718	Rat CDNA isolated
15	1311	95.9	1123	ABK34815	Rat CDNA isolated
16	1291.5	94.5	1927	AAK12584	Human protein havi
17	1259	92.1	810	AAK94076	Primer specific fo
18	1211	88.6	1792	AAK59230	Human polynucleoti
19	1208	88.4	1620	AAK59523	Human polynucleoti
20	1171	85.7	738	AAK64063	Human zacr3p3 degen
21	858.5	62.8	1799	AAK61016	Human polynucleoti
22	849	62.1	1608	ABK35221	Human CDNA encodin
23	721	52.7	471	AAK02874	Human secreted pro
24	721	52.7	472	AAK39551	Human secreted pro
25	513.5	37.6	546	AAK93419	CDNA encoding SRT
26	325	23.8	804	ABK35598	Gene encoding nove
27	316	23.1	1107	AAK61744	CDNA encoding rat
28	316	23.1	1107	AAK99677	Skin cell CDNA, SE
29	316	23.1	1107	ABK48329	Rat CDNA isolated
30	315	23.0	870	AAK16350	Human SBAKRP30a g
31	315	23.0	870	ABK08182	Human SBAKRP30a g
32	315	23.0	912	AAK16351	Human SBAKRP30a g
33	315	23.0	912	AAK99867	Human zacr3p CDNA,
34	315	23.0	1242	AAK44067	Human gensef metab
35	315	23.0	1297	ABK4966	Human novel polynu
36	313	22.9	855	AAK67788	Murine ACRP30RIM c
37	309	22.6	1282	AAK98975	Mouse zacr3p CDNA,
38	306	22.4	1052	AAK61811	CDNA encoding rat
39	306	22.4	1052	AAK99744	Skin cell CDNA, SE
40	306	22.4	1052	ABK34896	Rat CDNA isolated
41	306	22.4	1161	AAK65132	Human adipocyte co
42	306	22.4	1171	AAK31128	Human diagnostic a
43	306	22.4	1171	ABK04564	Human ovarian anti
44	304	22.2	932	AAK25606	CDNA encoding poly
45	299	21.9	1276	AAK51048	Murine adipocyte c

ALIGNMENTS

RESULT 1
ABK35591
ID ABR35591 standard; DNA, 741 BP.
XX
AC ABR35591:
XX
DT 08-MAY-2002 (first entry)
XX
DE Gene encoding novel human secreted or membrane-associated protein #10.
XX
XX Human; secreted protein; membrane-associated protein; hypertensive;
XX inflammatory disorder; neurological disorder; haematopoietic disorder;
XX skeletal developmental disorder; growth abnormality; autoimmune disorder;
XX neurodegenerative disorder; nervous system disorder; bacterial infection;
XX peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
XX hypotension; sexual development disorder; blood disorder; gene; ds.
XX Homo sapiens.

XX	PN	WO200204600-A2.
XX	PD	17-JAN-2002:
XX	PF	12-JUL-2001: 2001WO-US21985.
XX	PR	12-JUL-2000: 2000US-218033P.
XX	PR	21-AUG-2000: 2000US-226517P.
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	PA	(SMIK) SMITHKLINE BEECHAM PLC.
XX	PA	(GLAX) GLAXO GROUP LTD.
XX	P1	Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC,
XX	P1	Smith RF, Xiang Z, Xie Q;
DR	DR	WPI: 2002-188468/24.
XX	DR	P-PADB: AAU84371.
XX	PT	Novel secreted and membrane-associated polypeptides and polynucleotides
XX	PT	encoding the polypeptides, for preventing, treating and ameliorating
XX	PT	cancers, mental or sexual developmental disorders, and malignant tumours
PS	PS	Claim 2; Page 106; 151pp; English.
CC	CC	The present invention relates to the isolation of novel human secreted
CC	CC	or membrane-associated proteins and the genes encoding them. The
CC	CC	sequences of the invention are useful for treating, preventing and
CC	CC	ameliorating various diseases such as inflammatory disorders (e.g.
CC	CC	asthma), neurological disorders (e.g. dementia), haematopoietic
CC	CC	disorders, skeletal developmental disorders, growth abnormalities,
CC	CC	neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC	CC	disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC	CC	peripheral myelinopathies, viral and bacterial infections,
CC	CC	alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper-
CC	CC	lipotension, obesity, bulimia, anorexia, manic depression, delirium,
CC	CC	mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC	CC	or sexual development disorders, and dysfunctions of the blood cascade
CC	CC	system including those leading to stroke. ABK35582-ABK35609 represent
CC	CC	the genes encoding the novel human secreted or membrane-associated
CC	CC	proteins of the invention.
XX	SQ	Sequence 741 BP; 191 A; 178 C; 200 G; 172 T; 0 other:
<hr/>		
Alignment Scores:		
Pred. NO.:	7,45E-100	Length: 741
Score:	1367.00	Matches: 246
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	24	Gaps: 0
<hr/>		
SS-10-036-041-2 (1-246) x ABK35591 (1-741)		
QY	1	MettLeutrtPARgInLenuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
Dd	1	ATGCTTGAGAGCGACGCATCATTCATGGCAACTGCTGGCTTTGTTCCTCCCTTTTGC 60
QY	21	LeuysGlnAspGIuuyrMetGlnSerProGlnThrcllyGlyLeuProProAspCysser 40
Dd	61	CTGTGTCAAGATGAATCATGATGATCTCCACAAACCAGAGACTACCCCCAGACTGCAGT 120
QY	41	LysCysCysHISglYAspTYrSerPheArgGLyTyrGlnGlyProProGlyYPProProGly 60
Dd	121	AAGTGTTCATTCAGAGACTACAGCTTTCGAGCGACTCACCAAGGCCCTTGGGCCAACCGGGC 180
QY	61	ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
Dd	181	CCTCTGCGCATTCACGAGAACAACCATGAGAAACAATGCAACAATGAGACCACTGGTCATGAA 240
QY	81	GlyAlaIysGlyIuYrGlyAspLySGlyAspLeuclYProArGlyGluArGlyGln 100

D	b		241	GGAGCCAAAGGTGAGAACAGCGGCACAAAGTCACTGGGGCTCGAGGGAGCAGCGGGCAG	3000
O	y		101	HISGLIPROLYSGILGULYSLYTTPROCIYLIEPROGIULENGINLEALPHE	120
D	b		301	CATGACCCCAAGGAGAGAAGGCGTTACCCGGCATTCACACGAATTCCAGATTGCATTCC	360
O	y		121	METALASERLEUALATHHHSIPHERSERNINSNRSERYLIELLEPHESERSVAL	140
D	b		361	ATGGCTTCTCTGGCACCCACTTCAGCATACGAACAAGTGGAATTATCTTCAGCAGTCT	420
O	y		141	GLUTPRASNILEGLYSNPHEAPSPVLMETHRGIVARGPHEGLIALAIPROVALSER	160
D	b		421	GAGACCAACATTGGCAAATCTTTTGATGTCATGAGCTGTAATTTGGGCCACGATCA	480
O	y		161	GLYVALTYRPPHEPHERHPHESERMETMELYSHISGLIUSPSVALIGLIUVALTYRVAI	180
D	b		481	GGTGCTATTTCTTCACCTTCAGCATGATGANAAGATGAGATGTGTGAAGATGTATGTG	540
O	y		181	TYRLEUMETHIASNGLYASNTHVALPHESERMETYLSERTTRYGLUMETLYSGILYS	200
D	b		541	TACCTTATGCAACAATGGGACACAGCTCTTCAGCATGTGATGAACTGTGAAATGAAGGCGAAA	600
O	y		201	SERASPTRRSERSEARNHIALVALLEUNYSLLEUALYSLGILYAAPGIVALTTPLEU	220
D	b		601	TCAAGTACATTCACGAAATCATCTCTGCTGNAAGCTAGCCAAAGGGAGTAGAGTTGGCTG	660
O	y		221	ARGMETGLYASNGLYALAUENHISGLYSPHISGLINARGPHERSERTHRPEALAGLPHE	240
D	b		661	CGAATGGGCAATGGGCGCTCTCCATGSGGAGCACCAACGCTTCTCCACCTTGGCAGATTCC	720
O	y		241	LEULEUPHEGLUTHRLYS 246	
D	b		721	CTGCTCTTTGAAACTTAAG 738	
 RESULT 2 AAC64058 ID AAC64058 standard; cDNA, 1696 BP.					
A	C		AAC64058;		
D	T		19-FEB-2001 (first entry)		
D	E		Human zacrpf3 cDNA, SEQ ID NO:1.		
K	X		Human zacrpf3; adipocyte complement related protein homologue;		
K	W		ACRP3; C1q domain; collagen-like domain; energy balance modulation;		
K	V		cellular metabolism; metabolic disorder; obesity; anorexia;		
K	M		antimicrobial agent; infection; platelet aggregation inhibition;		
K	W		adhesion; activation; vascular injury; antibacterial; antiviral; ss.		
X	X		Homo sapiens.		
O	S		MO20006377-A1.		
N	N		26-OCT-2000.		
X	P		19-APR-2000; 2000MO-US10454.		
X	P		20-APR-1999; 99US-0294943.		
X	R		(ZYMO) ZYMOGENETICS INC.		
X	P		Piddington CS, Bishop PD;		
X	D		WPI: 2000-665243/64.		
X	R		P-PsDB: AAB29580.		
X	P		Novel zacrpf3 polypeptides used to treat or prevent bacterial or viral		
X	P		infections, for wound healing, improving blood flow, and to analyze		
X	P		energy efficiency in mammals -		
X	S		Claim 31; Page 107-109; 123pp: English.		

XX The invention relates to the human zacr3 protein (AAB29580) and to
CC nucleic acids which encode it (AAC64058, AAC64063). Zacr3 is a homologue
CC of adipocyte complement related protein (ACRP30) and contains a
CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
CC C-terminal C1q domain comprising 10 beta-strands. The zacr3 gene is
CC located on chromosome 5p12. The invention also relates to zacr3
CC fragments, fusion proteins containing zacr3 polypeptides,
CC zacr3-specific antibodies, expression constructs and host cells
CC comprising zacr3 nucleic acids, and methods of recombinant production of
CC zacr3. Human zacr3, and its agonists and antagonists may be used in the
CC study and modulation of cellular metabolism and energy balance in
CC mammals, and may therefore be used to treat disorders such as obesity and
CC anorexia, and conditions associated with these disorders. Due to its C1q
CC like domain, zacr3 and zacr3-containing fusion proteins may be useful
CC as anticlotting agents, promoting lysis or phagocytosis of infectious
CC organisms such as bacteria or viruses. Zacr3, its fragments, fusion
CC proteins, antibodies and activity modulators may also be used to inhibit
CC collagen-induced platelet aggregation, adhesion, or activation, and may
CC therefore have potential for promoting blood flow within the vasculature
CC of a mammal e.g., to treat injury to the vasculature or other collagenous
CC tissue. Human zacr3 and its antibodies may additionally be used to study
CC dimerisation and oligomerisation. The present sequence represents cDNA
CC encoding human zacr3.

XX Sequence 1696 BP; 482 A; 355 C; 386 G; 473 T; 0 other;

Alignment Scores:

Pred. No.:	1.94e-99	Length:	1696
Score:	1367.00	Matches:	246
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-036-041-2 (1-246) x AAC64058 (1-1696)

QY 1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys 20
DB 69 ATGCTTTGGAGCAGCCTCATTTGGCAACCTGCTGCTTTCTCTCTCTTTTGC 128
QY 21 LeuGlyGlnAspGluTyrMetGlnSerProGlnThrGlyGlyLeuProPheCysSer 40
DB 129 CTGTCGTAAGTGAATCATGAGTCTCCAAACCGAGGACTACCCCGACTGCAGT 188
QY 41 LysCysGlyHisGlyAspTyrSerPheArgGlyTyrGlnGlyProPheGlyProGly 60
DB 189 AAGGTTCATGAGTGAAGTACGCTTTCGAGCTACCAAGGCCCCCTGGCCACCGGCC 248
QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
DB 249 CCTCTGCGCATTTCCAGAAACCATGGAACATGAGCAACATGAGCAGCTGTCATGAA 308
QY 81 GlyAlaIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 309 GAGACCCAAAGGTGAAGGGGCGCAAAAGTCACTGGGGCTTCAGAGGGGCGCAG 368
QY 101 HisGlyProLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
DB 369 CATGGCCCCAAGAGAGAGAGAGGCTACCCGGGGATTCACACAGAACTTCACATTGCA 428
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal 140
DB 429 ATGGCTCTCTGGCAACCATCTCAGCAATCAGAAAGTGGAGTATCTTCAGCAGTGT 488
QY 141 GlnThrAsnIleGlyAsnPhePheAspValMetThrGlnArgPheGlyAlaProValSer 160
DB 489 GAGACCAACATTTGAATCTTTGATGTCATGACTGTAATTTGGGGCCCCGATATCA 548
QY 161 GlyAlaTyrPhePheThrPheSerMetMetLysHisGlnAspValGluGluValTyrVal 180
DB 549 GGTGTGATTTCTTCCACTTCAGCATGATGAGCATGAGATGTTGAGCAAGTGTATGTG 608

QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
DB 609 TACCTTATGGCAACATGGGACACAGTCTTCAGCATGTACACCTATGAATGAAAGGGC 668
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPhe 220
DB 669 TCAGTATCATCCAGCAATCATCTGTCTGTAAGCTAGCAAGGGGATGAGCTTTGGCTG 728
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
DB 729 CGAATGGGCATTTGGCGCTCTCCATAGGGGACCAAGGCTTCTCAGCTTTCAGAGATTC 788
QY 241 LeuLeuPheGluThrLys 246
DB 789 CTGCTTTTGAAGTAAG 806
RESULT 3
ID AAF93874 standard; cDNA: 1709 BP.
XX AAF93874:
AC AAF93874:
XX 23-MAY-2001 (first entry)
DE Human cDNA encoding a membrane or secretory protein clone PSEC0232.
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KM Rheumatoid arthritis; diabetes; ss.
XX Homo sapiens.
XX EP1067182-A2.
PD 10-JAN-2001.
XX 07-JUL-2000; 2000EP-0114090.
PF 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX (HELI-) HELIX RES INST.
PA Oka T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
PI WPI: 2001-093989/11.
DR P-PSDB; AAB88447.
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -
XX Claim 1; SEQ ID 261; 609pp + CD ROM, English.
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAB88317 - AAB88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies (agonists and antagonists) may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also

CC dermatitis herpeticiformis or Crohn's disease. The nucleic acids may be used
 CC to generate transgenic animals for use in development and screening of
 CC therapeutically useful reagents and also for chromosome identification
 CC and tissue typing.

XX Sequence 1712 BP; 491 A; 358 C; 388 G; 475 T; 0 other;

Alignment Scores:

Pred. No.:	1.96e-99	Length:	1712
Score:	1367.00	Matches:	246
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-10-036-041-2 (1-246) x AAA96336 (1-1712)

OY 1 MetLeuTPATGGLnLeuLlETyTTPGlnLeuAlaLeuPhePheLeuProPheCys 20
 Db 77 ATGCTTGGAGGCACTATCTATTGGCACTCGGCTTTTCTTCTTCTTCTTCTTTC 136
 OY 21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
 Db 137 CTGTGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
 OY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
 Db 197 AAGTCTTCATGTGAGCTACAGCTTTCAGAGCTACCAAGGCCCCCTGGGGCCAGCGGC 256
 OY 61 PropGlyIleProGlyIleProGlyIleProGlyIleProGlyIleProGlyIleProGly 80
 Db 257 CCTCTGGCATTCAGGAAACCATGAAACATGAAACATGAAACATGAAACATGAAACAT 316
 OY 81 GlyAlaLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
 Db 317 GGAGCCAAAGGCGAAGAGGCGAAGAGGCGAAGAGGCGAAGAGGCGAAGAGGCGAAG 376
 OY 101 HisGlyProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
 Db 377 CATGGCCCCAAGAGAGAGAGGCGTACCCGGGATTCACCAAGAACTTCAGATTCATTC 436
 OY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
 Db 437 ATGGCTTCTCTGCGCAACCACTTCGCAATCAGAACATGGGATTAATCTTCAGCACTGT 496
 OY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
 Db 497 GAGACCACATTTGGAACCTCTTTGATGTCATGACTGGTAGATTGGGGCCCCAGATATCA 556
 OY 161 GlyValIYrPhePheThrPheSerMetMetIlySHISGluAspValGluGluValIYrVal 180
 Db 557 GGTGTGTATTTCTTCCACTTCAGCATGATGAAGCATGAGGAGTGTGAGAGATGATATG 616
 OY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetIYrSerTyrGluMetIlyGlyIly 200
 Db 617 TACCTTAATGCAATGAGCAACACACTCTTCACATGTCACAGCTATGAATGAAAGGGCA 676
 OY 201 SerAspThrSerSerAsnHisAlaValLeuIlyLeuAlaIlyGlyAspGluValIYrPhe 220
 Db 677 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTGGCG 736
 OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
 Db 737 CGAAGGGCAATGGCGCTTCATGCGAGGAGCCACCAAGCTTCTCCACCCTTCAGAGATTC 796
 OY 241 LeuLeuPheGluThrIly 246
 Db 797 CTGCTCTTTGAACATAAG 814

RESULT 5
 AAA95787
 ID AAA95787 standard; cDNA; 1760 BP.

AC AAA95787:
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human immune system molecule cDNA from Incyte clone 1890540.
 XX

KW Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;
 KW antiarteriosclerotic; antisthmatic; antidiabetic; nephrotoxic; cancer;
 KW antigout; dermatological; antihypertensive; antiviral; hepatotropic; antibody;
 KW immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;
 KW gene therapy; diagnostic; immunological disorder; viral infection; ss;
 XX bacterial infection; fungal infection; parasitic infection; immunogen.

OS Homo sapiens.
 XX
 PN WO200060080-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 04-APR-2000; 2000WO-US09072.
 XX
 PR 05-APR-1999; 99US-0127852.
 XX
 PR 05-MAY-1999; 99US-0132647.
 XX

PA (INCYTE) INCYTE PHARM INC.
 XX
 PI Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DM;
 XX
 DR WPI: 2000-665005/64.
 DR P-PSDB: AAB15548.
 XX

PT New human immune system molecules 1-15 and polynucleotides encoding
 PT them useful for diagnosing, treating or preventing e.g. immunological
 PT disorders, infections, cell proliferative disorders, microbial
 PT infections -
 XX

PS Claim 4; Page 93; 95pp; English.

XX This sequence represents the cDNA for a human immune system molecule
 CC (IMOL) isolated as clone 1890540 from the Incyte BLADRV07 library.
 CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides
 CC (AAA95775-A95789), and compositions comprising them are useful for the
 CC diagnosis, treatment or prevention of immunological disorders,
 CC infections and cell proliferative disorders, including cancer. The IMOL
 CC may be used to treat or prevent disorders associated with decreased
 CC expression or activity of IMOL, such as immunological disorders
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
 CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
 CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.
 CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
 CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
 CC useful as immunogens for the development of antibodies that
 CC specifically recognizes these peptides. The polynucleotides may be used
 CC to detect and quantify gene expression in biopsied tissues in which
 CC expression of IMOL may be correlated with the disease, as targets in a
 CC microarray, to detect differences in gene sequences among normal,
 CC carrier and affected individuals, and for screening libraries of
 CC compounds in drug screening techniques. Antibodies which specifically
 CC bind to IMOL may be used for the diagnosis of disorders characterized
 CC by expression of IMOL, or in assays to monitor patients being treated
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.
 CC
 XX

SQ Sequence 1760 BP; 505 A; 376 C; 395 G; 484 T; 0 other;

Alignment Scores:
 Pred. No.: 2.02e-99
 Score: 1367.00
 Percent Similarity: 100.00%
 Best local Similarity: 100.00%
 Query Match: 100.00%
 DB: 21
 Length: 1760
 Matches: 246
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-036-041-2 (1-246) x AAA95787 (1-1760)

```
QY 1 MetLeuTrpArgGlnLeuIleTyrrTrpGlnLeuAlaLeuPheLeuPropheCys 20
DB 124 ATGCTTTGGAGGAGCTCATCTATTTGGCAACTGCTGCTTTGTTTCTCCCTTTTGC 183
QY 21 LeuCySGlnAspGluTyrMetGluSerProGluThrGlyGlyLeuPropheAspCysSer 40
DB 184 CTGTGTCAAGATGAATACATGAGAGTCTCCCAAAACCGAGAGACTACCCCAAGACTGACT 243
QY 41 LysCySGlyHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
DB 244 AAGTGTTCATGAGAGACTGACCTTTCGAGGCTACCAAGGCCCTTGGGCCACCGGGC 303
QY 61 ProProGlyTyrLeuProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
DB 304 CCTCTGGCATTCACAGAAACCATGAAACAAATGCAACATGAGAGCCACTGGTCATGAA 363
QY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLysGlyProArgGlyGlyAlaGlyGln 100
DB 364 GAGGCCAAAGGTAGAGAGGCGCAAAAGGTGACCTGGGCTTGGAGGGAGGCGGAG 423
QY 101 HisGlyProLysGlyGlyLysGlyTyrProGlyTyrLeuProProGlyLeuGlnIleAlaPhe 120
DB 424 CATGGGCCCAAGAGAGAGAGGAGGCTACCGGGGATTCACAGAACTTCAGATTGCAATTC 483
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
DB 484 ATGGCTTCTGTGGCAACCCACTTCACCAATCAACAGAGTGAGTTATCTTCACACAGCTT 543
QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
DB 544 GAGACCAACATTTGAAACTCTTTGATGTCATACCTGCTGATTTGGGCCCAAGATCA 603
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
DB 604 GGGTGTATTTCTTCACTTACATGATGATGATGATGATGATGATGATGATGATGATGATG 663
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
DB 664 TACCTTATGACATGAGCAACAGTCTTCAGCATGTACAGCTATGAATAAGAGGGCAAA 723
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
DB 724 TCAGATACATTCAGCAATCATGCTGTGCTGAGACTAGCCAAAGGATGAGTTGGCTG 783
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
DB 784 CGAATGGCAATGGCGCTCTCCATGGGACACACACGCTTTCACACTTTCGAGGATTC 843
QY 241 LeuLeuPheGluThrLys 246
DB 844 CTGCTCTTTGAAACTAAG 861

RESULT 6
ABK35590
ID ABK35590 standard; DNA; 960 BP.
XX
XX ABK35590;
08-MAY-2002 (first entry)
DE Gene encoding novel human secreted or membrane-associated protein #9.
XX
XX Human; secreted protein; membrane-associated protein; hypertension;
XX inflammatory disorder; neurological disorder; haematopoietic disorder;
XX skeletal developmental disorder; growth abnormality; autoimmune disorder;
XX neurodegenerative disorder; nervous system disorder; bacterial infection;
XX peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
XX hypotension; sexual development disorder; blood disorder; gene; ds.
OS Homo sapiens.
```

```
XX
PN WO200204600-A2.
XX
XX 17-JAN-2002.
XX
XX 12-JUL-2001; 2001WO-US21985.
XX
XX 12-JUL-2000; 2000US-218033P.
XX 21-AUG-2000; 2000US-226517P.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX (SMK ) SMITHKLINE BEECHAM PLC.
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC,
XX Smith RF, Xiang Z, Xie Q;
XX WPI; 2002-188468/24.
XX P-P-SDB; AAU84370.
XX
XX Novel secreted and membrane-associated polypeptides and polynucleotides
XX encoding the polypeptides, for preventing, treating and ameliorating
XX cancers, mental or sexual developmental disorders, and malignant tumours
XX
XX Claim 2; page 106; 151pp; English.
XX
XX The present invention relates to the isolation of novel human secreted
XX or membrane-associated proteins and the genes encoding them. The
XX sequences of the invention are useful for treating, preventing and
XX ameliorating various diseases such as inflammatory disorders (e.g.
XX asthma), neurological disorders (e.g. dementia), haematopoietic
XX disorders, skeletal developmental disorders, growth abnormalities,
XX neurodegenerative disorders (e.g. Huntington's disease), nervous system
XX disorders, autoimmune disorders (e.g. rheumatoid arthritis),
XX peripheral myelinopathies, viral and bacterial infections,
XX alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
XX hypopension, obesity, bulimia, anorexia, manic depression, delirium,
XX mental retardation, Tourette's syndrome, schizophrenia, growth, mental
XX or sexual development disorders, and dysfunction of the blood cascade
XX system including those leading to stroke. ABK35582-ABK35609 represent
XX the genes encoding the novel human secreted or membrane-associated
XX proteins of the invention.
XX
XX Sequence 960 BP; 261 A; 232 C; 262 G; 205 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 4.94e-96 Length: 960
XX Score: 1320.50 Matches: 246
XX Percent Similarity: 77.128 Conservatve: 0
XX Best Local Similarity: 77.128 Mismatches: 0
XX Query Match: 96.608 Indels: 73
XX DB: 24 Gaps: 1
XX
XX US-10-036-041-2 (1-246) x ABK35590 (1-960)
QY 1 MetLeuTrpArgGlnLeuIleTyrrTrpGlnLeuAlaLeuPheLeuPropheCys 20
DB 1 ATGCTTTGGAGGAGCTCATCTATTTGGCAACTGCTGCTTTGTTTCTCCCTTTTGC 60
QY 21 LeuCySGlnAspGluTyrMetGlu
DB 61 CTGTGTCAAGATGAATACATGAGAGTCTCCCAAAACCGAGAGACTACCCCAAGACTGACT 120
QY 28
DB 121 GTCGAAGCAGCAGCAGAGACTGGCGCTCAGCGGCTCCAGAGAGGAGAGAAAGTGAAGAGCGG 180
QY 28
DB 181 AGGCATCTAAAACTGGAGCTGTGATTAATACACTTTCACAGACCTAAATCCCTGAGA 240
QY 28
```

DB 241 CCAGATGACCTACCCGAGTAGATGACCTAGCCAGATCACCACATTCCTGGGCC 300
 QY 29 ----SerProGlnThnGlyLeuProProAspCysSerIleCysHisGlyAspTyr 47
 DB 301 CAGTCTCCCAAAACGAGGAGCTACCCGAGACTGCAGACTGCAAGGTTGTCATGAGAGCTAC 360
 QY 48 SerPheArgIleTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
 DB 361 AGCTTCCGAGGCTACCAAGGCCCTGGGCCACCGGGCTCTGCGCATTCAGAGAAAC 420
 QY 68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlyAlaAlaGlyGlyIleGlyGly 87
 DB 421 CATTGAAACAAATGCAACATGAGGAGCCACTGGCATGATGAGAGGCCAAAGTGAAGAGGCC 480
 QY 88 AspIleGlyAspLeuGlyProArgGlyIleArgGlyGlyHisGlyGlyProGlyGlyGly 107
 DB 481 GACAAAGGTGACCTGGGGCTCGAGGGAGCGGGGACCATGGCCCAAAAGAGAGAG 540
 QY 108 GlyTyrProGlyIleProProGlyLeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
 DB 541 GGTACCCCGGAGTTCCACAGAACTTCAGATTGCTTCATGCTTCTCTGCGCAACCCAC 600
 QY 128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsn 147
 DB 601 TTCAGCAATCAGAACAGTGGATTTATCTTCAGCAGTGTGAGACCAACATGGAACTTC 660
 QY 148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
 DB 661 TTTGAGTGTATGATGCTGTGATTTGGGGCCCAAGTACAGGTGTGATTTCTTCACCTTC 720
 QY 168 SerMetMetLeuHisGlyAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
 DB 721 AGCATATGACATGAGATGATGTGAGAGATGATGTGATGCTTATGACATGGCAAC 780
 QY 188 ThrValPheSerMetCysSerTyrGluMetLeuGlyLysSerAspThrSerSerAsnHis 207
 DB 781 ACAGTCTTACAGCATGTACAGCTATGAAATGAAAGGCCAAATCAGATCAGCAATCAT 840
 QY 208 AlaValLeuLeuLeuAlaGlyAspGlyValTyrLeuArgMetLeuGlyAsnGlyAlaLeu 227
 DB 841 GCTGTCTGAGCTACCAAGGGATGAGGTTGGCTGGAATGGCAATGGCGCTCTTC 900
 QY 228 HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluThrLys 246
 DB 901 CATTGGGACCAACAGCTTCTCCACTTTCAGAGATTCCTGCTTTGAACATAAG 957
 RESULT 7
 AAC99776
 ID AAC99776 standard; cDNA; 1035 BP.
 AC AAC99776;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Skin cell cDNA, SEQ ID NO: 424.
 XX
 KW Rat; skin cell; cytosolic; anti-inflammatory; anti-HIV;
 KW neutrotropic; neuroprotective; antiviral; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
 KW inflammation; neurological disease; ss.
 XX
 OS Rattus sp.
 XX
 PN WO200069884-A2.
 PD 23-NOV-2000.
 XX
 PF 15-MAY-2000; 2000MO-N200075.
 XX
 PR 14-MAY-1999; 99US-0312283.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.

XX
 PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
 XX WPI: 2001-007495/01.
 DR P-PSDB: AAB55908.
 XX
 PT New isolated polynucleotide used in the identification of genetic
 PT disorders and encoding polypeptides used for treating inflammatory
 PT disease, cancer and neurological diseases -
 XX
 PS Claim 1: Page 317-318; 352pp; English.
 XX
 CC The present polynucleotide encodes a polypeptide which is expressed in
 CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
 CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.
 XX
 SQ Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other:
 Alignment Scores:
 Pred. No.: 3,06e-95 Length: 1035
 Score: 1311.00 Matches: 236
 Percent Similarity: 97.15% Conservative: 3
 Best Local Similarity: 95.93% Mismatches: 7
 Query Match: 95.90% Indels: 0
 DB: 22 Gaps: 0
 US-10-036-041-2 (1-246) x AAC99776 (1-1035)
 QY 1 MetLeuTrpArgGlnIleuIleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCys 20
 DB 92 ANGCTCAGAGGAGGAGCTCGCTCGTGGTGGACCTGCTGCTTTCCTCCATTTTTC 151
 QY 21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
 DB 152 CTGTGCAAGATGAATACATGAGCTCTCCACAGCTGGAGAGATGCCCCACAGCTGACG 211
 QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
 DB 212 AGTGTTGCCATGAGATATATGATTCGCGGTACCAAGGCCCTGGACCCCAAGCT 271
 QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
 DB 272 CCTCCGCGCATTCACAGAAACCATGGAACAAATGAAATACAGGACCATGGCCACGAA 331
 QY 81 GlyAlaLeuGlyGlyLeuGlyAspLeuGlyAspLeuGlyProArgGlyIleArgGlyGln 100
 DB 332 GGGGCCAAGGTGAGAAAGAGACAAAGGCGACTGGGGCTCGAGGGAGACGGGGCAG 391
 QY 101 HisGlyProLysGlyLeuLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
 DB 392 CATGGCCCCAAAGATGAGAAAGGATACCCAGGGGTGCGACCAAGCTCGCATTCGCTTC 451
 QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal 140
 DB 452 ATGGCTTCTAGCGACTCCTCACCAATCAGAACAGTGGCTTATTCCTCACAGCTTT 511
 QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
 DB 512 GAGACCAACATGGAACCTTCTCGATGTCATGATGATTTGGGGCCCGCGATCA 571
 QY 161 GlyValTyrPhePheThrPheSerMetMetLeuHisGlyAspValGluGluValTyrVal 180
 DB 572 GCGGTATTTTCTTCACCTTCACATGATGATGATGAGAGAGAGAGAGATGATG 631
 QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200

PS Claim 1; Page 73; 235pp; English.

XX The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AA261606-261817 represent cDNA sequences derived
 CC from several mouse, rat or human skin cell types. Sequences
 CC AA261606-261649, AA261725-261765, AA261802-261811 and AA261826 encode
 CC proteins with an N-terminal signal sequence, indicating that the proteins
 CC are secreted. Sequences AA261650-261668, AA261766-261780, AA261812-261817
 CC and AA261827-261829 encode proteins with one or more putative
 CC transmembrane domains.

XX Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

SQ

Alignment Scores:

Pred. No.:	3,36e-95	Length:	1123
Score:	1311.00	Matches:	236
Best Similarity:	97.15%	Conservative:	3
Best Local Similarity:	95.93%	Mismatches:	7
Query Match:	95.90%	Indels:	0
DB:	21	Gaps:	0

US-10-036-041-2 (1-246) x AA261633 (1-1123)

QY 1 MetLeuTrpArgGlnLeuIleTyrTTPGlnLeuAlaLeuPheLeuProPheCys 20
 DB 180 ATGCTCAGGAGGCGAGCTGCTGCTGCGACCTGCTGCTTTCTCCATTTTGC 239

QY 21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
 DB 240 CTGTGTAAAGTAAATGATGAGTCTCCACAACTGAGAGAGCCGCCACAGCTGAGC 299

QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProGly 60
 DB 300 AAGTGTGCCATGAGATTTATGATTCCTCGTGTACCAAGGCCCTTGAGCCGCCAGGT 359

QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
 DB 360 CCTCTGTCATTCCTCAGAAACCATGAAACAATGAAATTAACGAGGACCTGCGACGAA 419

QY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyGlyArgGlyGln 100
 DB 420 GGGGCCAAGGAGTGAAGAAAGAGACAAAGGCGACCTGGGCTCGAGGGGAAACGGGGCAG 479

QY 101 HisGlyProLysGlyGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
 DB 480 CATGGCCCCAAGATGAAAGGAGTACCCAGGGGTGCCACCAAGCTGCGAGATTGCGTTTC 539

QY 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal 140
 DB 540 ATGGCTCTCTAGAGCACTCACTCAGCAATCAGACAGTGCATATTATCTTCAGACAGTGT 599

QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
 DB 600 GAGGCAACATTTGAAACTTCTTCGATGTCATGCTGTGATTTGGGGCCCCCGTATCA 659

QY 161 GlyValTyrPhePheThrPheSerMetCysHisGlyAspValGluGluValTyrVal 180
 DB 660 GCGCTGATTTCTTCCACTTCAGCATATGACATGAGACGCGGAGGAAGTATATGTG 719

QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
 DB 720 TACCTTATGCAACATGATGTAACACGCTGTCAGCATGTGTAACAAGAGGAAAA 779

QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrLeu 220

DB 780 TCAGATACATCCAGCAACCATGCACTGCTGAAGTTGGCCAAAGAGATGAACTCGGCTA 839

QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaIlePhe 240
 DB 840 AGAATGGGCAACGGTGGCCCTCATGGGACACACAGCCCTTCTACCTTGGCAGGCTTT 899

QY 241 LeuLeuPheGluThrLys 246
 DB 900 CTGCTTTTTCGAACTAAG 917

RESULT 11
 AA261730
 ID AA261730 standard; cDNA; 1123 BP.
 XX
 AC AA261730;
 XX
 DT 27-MAR-2000 (first entry)

DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:203.
 XX
 XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
 XX
 OS Rattus sp.
 XX
 PN MO9955865-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99MO-NZ00051.
 XX
 PR 29-APR-1998; 98US-0069726.
 PR 09-NOV-1998; 98US-0188930.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PI Strachan L, Sleeman M, Watson JD, Omrust R, Kumble A, Murison JG;
 DR WPI; 2000-072177/06.
 DR P-PSDB; AAY76025.
 PT Novel polynucleotides useful for the treatment of various conditions
 including wounds and cancer -
 XX
 PS Claim 1; Page 137; 235pp; English.

XX The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AA261606-261817 represent cDNA sequences derived
 CC from several mouse, rat or human skin cell types. Sequences
 CC AA261606-261649, AA261725-261765, AA261802-261811 and AA261826 encode
 CC proteins with an N-terminal signal sequence, indicating that the proteins
 CC are secreted. Sequences AA261650-261668, AA261766-261780, AA261812-261817
 CC and AA261827-261829 encode proteins with one or more putative
 CC transmembrane domains.

SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:
 Pred. No.: 3,36e-95 Length: 1123

Score:	1311.00	Matches:	236
Percent Similarity:	97.15%	Conservative:	3
Best Local Similarity:	95.938	Mismatches:	7
Query Match:	95.908	Indels:	0
DB:	21	Gaps:	0

US-10-036-041-2 (1-246) x AAZ61730 (1-1123)

[illegible]

XX	KM	Inflammation; neurological disease; ss.
XX	OS	Rattus sp.
XX	PN	WO200069884-A2.
XX	PD	23-NOV-2000.
XX	PF	15-MAY-2000; 2000MO-NZ00075.
XX	PR	14-MAY-1999; 99US-0312283.
XX	PA	(GENE-) GENESIS RES & DEV CORP LTD.
XX	PI	Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison J
XX	DR	WPI: 2001-007495/01.
XX	DR	P-PSDB: AAB55908.
XX	PT	New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
XX	PS	Claim 1; Page 87; 352pp; English.
XX	CC	The present polynucleotide encodes a polypeptide which is expressed i
XX	CC	mammalian skin cells. The polypeptide is useful for stimulating
XX	CC	keratinocyte growth and motility, inhibiting the growth of cancer cel
XX	CC	modulating angiogenesis, inhibiting angiogenesis and vascularisation
XX	CC	tumours, modulating skin inflammation, stimulating the growth of
XX	CC	epithelial cells, inhibiting the binding of human immunodeficiency vi
XX	CC	(HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
XX	CC	neurological diseases. The polynucleotide can be used as a marker, in
XX	CC	the identification of genetic disorders, and for the design of
XX	CC	oligonucleotides for examining expression patterns.
SO		Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;
		Alignment Scores:
		Pred. No.: 3,36e-95 Length: 1123
		Score: 1311.00 Matches: 236
		Percent Similarity: 97.15% Conservative: 3
		Best Local Similarity: 95.93% Mismatches: 7
		Query Match: 95.90% Indels: 0
		DB: 22 Gaps: 0
		US-10-036-041-2 (1-246) x AAC99566 (1-1123)
QY	1	MettLeuTPtArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPheIleuProPheCys 20
DB	180	ATGCTCAGAGGACACCTGCTGGGAGCACCCTGGCTTGGCTTCTCCACATTTTGC 239
QY	21	LeuCysGlnAspGluTyrMetGluSerProGlnIhrGlyGlyLeuProProAspCysSer 40
DB	240	CTGTCTCAGATGAATACATGAGCTCTCCACAACCTGAGAGACTGCCCCACACTGCAGC 299
QY	41	LYSCYSCYSHISGLYASPTYSerPheArgGlyTyrGlnGlyProProGlyIleProProGly 60
DB	300	AAGGTGTGCCATGAGGATTAATGATTCGCTGCTGATTCACAGAGGCCCTCGAGACCCCAAGT 359
QY	61	ProProGlyIleProGlyAsnHisGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaIhrGlyHisGlu 80
DB	360	CTCTCTGGCATTCACGAAACCATGGAACAATGGAATAACGAGACCTGGGCCACGAA 419
QY	81	GlyAlaIhrGlyGlyLeuGlyGlyAspGlyGlyAspGlyGlyProArgGlyGlyIhrGlyGln 100
DB	420	GGGGCCCAAGGTGAAGAAAGGAGACAAAGGCACTGGGGCTCGAGGGGAACGGGGCAG 479
QY	101	HisGlyProLYSGlyGlyGlyGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
DB	480	CATGGCCCCAAGGATAGAGAGGATACCCAGGGGTCCACCAAGAGCTGCAGATTGGCTTC 539
QY	121	MetaIaSerLeuAlaIhrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal 140

|||||
Db 540 ATGGCTTCTTACGAGCTCTTACGACATCAACAGAGTGGCTTATCTTACAGAGGTT 539
QY 141 GluThrAsnIleGlyAsnPhenAspValMetThrGlyArgPheGlyAlaProValSer 160
Db 600 GAGACCAACATGTGAACCTCTTCGATGTCATGATGATGATGGGCCCCGATCA 659
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
Db 660 GGGGTGATTTCTTCACTTCACATGATGATGATGATGATGATGATGATGATGATG 719
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
Db 720 TACCTTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 779
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
Db 780 TCAGATGATCATGCAACCATGATGATGATGATGATGATGATGATGATGATGATGATG 839
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
Db 840 AGATGGGCAACGGTCCCTCCATGGGAGCACACAGCGCTTCTCTACCTTCGACAGGCTTT 899
QY 241 LeuLeuPheGluThrLys 246
Db 900 CTCCTTTTGAACATAAG 917
RESULT 13
AAC99663
ID AAC99663 standard; cDNA; 1123 BP.
XX
AC AAC99663;
XX
DT 08-MAR-2001 (first entry)
XX
DE Skin cell cDNA, SEQ ID NO: 203.
XX
XX Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KM neutropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KM inflammation; neurological disease; ss.
XX
OS Rattus sp.
XX
XX WO200069884-A2.
XX
XX 23-NOV-2000.
XX
PD 15-MAY-2000; 2000MO-NZ00075.
XX
PF 14-MAY-1999; 9905-0312283.
XX
PR (GENE-) GENESIS RES & DEV CORP LTD.
XX
PA Watson JD, Strachan L, Orust R, Sleeman M, Kumble KD, Murlison JG;
PI WPI; 2001-007495/01.
DR P-PSDB; AAB55958.
XX
XX New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -
XX
XX Claim 1; Page 176-177; 352p; English.
XX
XX The present polynucleotide encodes a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in

CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.
XX
SQ Sequence 1123 BP: 277 A; 266 C; 321 G; 258 T; 1 other;
Alignment Scores:
Pred. No.: 3 36e-95 Length: 1123
Score: 1311.00 Matches: 236
Percent Similarity: 97.15% Conservative: 3
Best Local Similarity: 95.93% Mismatches: 7
Query Match: 95.90% Indels: 0
DB: 22 Gaps: 0
US-10-036-041-2 (1-246) x AAC99663 (1-1123)
QY 1 MetLeuTrrPargLInleuLleTrrTrrGlnLeuLeuAlaLeuPheLeuPropheCys 20
Db 180 ATGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 239
QY 21 LeuGlyGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
Db 240 CTGTGCAAGATGAATACATGAGTGTCCACAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 299
QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
Db 300 AAGTGTGTCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 359
QY 61 ProProGlyLleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
Db 360 CCTCGGCGATTCACAGAAACCATGCAACATGAAATGACGAGGAGGAGGAGGAGGAGGAGG 419
QY 81 GlyAlaLysGlyLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
Db 420 GGGGCCAAGGAGTGAAGAGAGCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
QY 101 HisGlyProLysGlyLysGlyTyrProGlyLleProProGlyLeuGlnIleAlaPhe 120
Db 480 CATGGCCCCAAGAGATGAGAGGATGACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyLleIlePheSerSerVal 140
Db 540 ATGCTTCTCTACGAGCTCACTCAGCAATCAGACAGTGGATTTATCTTCACAGAGTGT 599
QY 141 GluThrAsnIleGlyAsnPhenAspValMetThrGlyArgPheGlyAlaProValSer 160
Db 600 GAGACCAACATGTGAACCTCTTCGATGTCATGATGATGATGATGATGATGATGATGATG 659
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
Db 660 GGGGTGATTTCTTCACTTCACATGATGATGATGATGATGATGATGATGATGATGATG 719
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
Db 720 TACCTTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 779
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
Db 780 TCAGATGATCATGCAACCATGATGATGATGATGATGATGATGATGATGATGATGATG 839
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
Db 840 AGATGGGCAACGGTCCCTCCATGGGAGCACACAGCGCTTCTCTACCTTCGACAGGCTTT 899
QY 241 LeuLeuPheGluThrLys 246
Db 900 CTCCTTTTGAACATAAG 917
RESULT 14
ABL34718
ID ABL34718 standard; cDNA; 1123 BP.
XX
XX ABL34718;
XX

DT 04-APR-2002 (first entry)
XX Rat cDNA isolated from skin cells SEQ ID NO: 28.
DE
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
XX developmental defect; inflammatory disease; dermatological; vulnery;
XX immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
XX ss.
OS Rattus sp.
XX WO200190357-A1.
PN
PD 29-NOV-2001.
XX 24-MAY-2001; 2001WO-NZ00099.
PF
XX 24-MAY-2000; 2000US-206650P.
PR
XX 25-JUL-2000; 2000US-221232P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
XX WPI: 2002-122020/16.
DR
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -
XX
PS Claim 1; Page 86-87; 466pp; English.
XX
XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC cDNA of the invention.
XX
SO Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other:

Alignment Scores:
Pred. No.: 3.36e-95 Length: 1123
Score: 1311.00 Matches: 236
Percent Similarity: 97.15% Conservative: 3
Best Local Similarity: 95.93% Mismatches: 7
Query Match: 95.90% Indels: 0
DB: 24 Gaps: 0.

US-10-036-041-2 (1-246) x ABL34718 (1-1123)
OY 1 MetLeuTPaYgInLeuIleTyTrrpGInLeuAlaLeuPhePheLeuProPheCyS 20
DB 180 ATGCTCAGAGGACCTGCTGCTGGCGACCTGGCTTCTTTCTTCTCCCATTTTTC 239
OY 21 LeuCySGInAspGlyTyrMetGInSerProGInThrGlyLeuProPhePheSer 40
DB 240 CTGTGTCAAGATGATCTGAGTCTCCACAACTGGAGGAGCTGCCCACTGACAC 299
OY 41 LysCySGInAspGlyTyrMetGInSerPheArgGlyTyrGInGlyProProGlyProGly 60
DB 300 AAGTGTGCGCATGAGATATGATTCCTGTTACCAAGGAGCCCTGACCCAGGT 359
OY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGly 80
DB 360 CCTCTGGCATTCAGAAACCAATGGAACCAATGGAACCAATGGAACCAATGGAACCA 419
OY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLysGlyAspLysGlyAspLysGlyGln 100
|||||

DB 420 GGGCCCAAGGTGAGAAAGAGACAAAGGCGACCTGGGCTCTGAGGAGGAGCGAG 479
OY 101 HisGlyProLysGlyGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
DB 480 CATGGCCCCCAAGGATAGAACGATACCAGGGGTGCCACAGAGCTGAGATTGGCTTC 539
OY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal 140
DB 540 ATGGCTTCTCTAGCGACTACTTCAGCAATCAGAACAGTGGCATTTATCTTCAGCACTGT 599
OY 141 GluThrAsnIleGlyAsnAspPheAspValMetThrGlyArgPheGlyAlaProValSer 160
DB 600 GAGACCAACATTGGAACACTTTCGATGTCATGACATGATGATTTGGGCCCCCATCA 659
OY 161 GlyValTyrPhePheThrPheSerMetLysHisGlyAspValGluValTyrVal 180
DB 660 GCGGTATTTCTTCCCTTCAGCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
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DB 720 TACCTTATGCAAAATGATGACAGGCTTTCAGCATGATGATGATGATGATGATGATGAT 779
OY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrLeu 220
DB 780 TCAGATACATCCAGACACATGCTGAGAGTTGCCCAAGAGATGATGATGATGATGATGAT 839
OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
DB 840 ACAATGGCCAAAGCGTCCCTCATGGGAGCACACAGCGCTCTCTACCTTCGACAGCTTT 899
OY 241 LeuLeuPheGlyLys 246
DB 900 CTGCTTTTGAACCTAAG 917

RESULT 15
ID ABL34815 standard; cDNA; 1123 BP.
AC ABL34815;
XX
XX 04-APR-2002 (first entry)
DE
XX Rat cDNA isolated from skin cells SEQ ID NO: 203.
XX
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
XX developmental defect; inflammatory disease; dermatological; vulnery;
XX immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
XX ss.
OS Rattus sp.
XX WO200190357-A1.
PN
PD 29-NOV-2001.
XX 24-MAY-2001; 2001WO-NZ00099.
PF
XX 24-MAY-2000; 2000US-206650P.
PR
XX 25-JUL-2000; 2000US-221232P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
XX WPI: 2002-122020/16.
DR
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -
XX
PS Claim 1; Page 155-156; 466pp; English.

CC The present invention provides the protein and coding sequences of cDNAs
 CC isolated from human, murine and rat skin cell libraries. The sequences
 CC can be used in the development of therapeutic agents useful in the
 CC treatment of skin diseases, including skin wounds, cancer, growth
 CC defects, developmental defects and inflammatory diseases. The proteins
 CC have important roles in the induction of hair growth, cell proliferation
 CC and cell-cell interaction, in maintaining tissue integrity, in wound
 CC healing and in modulating immune responses. The present sequence is a
 CC cDNA of the invention.

XX
 SQ Sequence 1123 BP: 277 A; 266 C; 321 G; 258 T; 1 other;

Alignment Scores:

Pred. No.:	3,36e-95	Length:	1123
Score:	1311.00	Matches:	236
Percent Similarity:	97.15%	Conservative:	3
Best Local Similarity:	95.93%	Mismatches:	7
Query Match:	95.90%	Indels:	0
DB:	24	Gaps:	0

US-10-036-041-2 (1-246) x ABL34815 (1-1123)

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QY 21 LeuCGSInAspGIuTYrMetGIuSerProGIuThrGIuLeuProProAspCysSer 40
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QY 241 LeuLeuPheGIuThrLys 246
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Search completed: January 15, 2003, 19:51:11
 Job time : 304 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 15, 2003, 19:41:40 ; Search time 71 Seconds
(without alignments)
1062.570 Million cell updates/sec

Title: US-10-036-041-2
Perfect score: 1367
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1311	95.9	1123	3 US-09-188-930-28	Sequence 28, App1
2	1311	95.9	1123	3 US-09-188-930-203	Sequence 203, App1
3	316	23.1	1107	3 US-09-188-930-217	Sequence 217, App1
4	299	21.9	1276	2 US-08-463-911-1	Sequence 1, App1
5	293.5	21.5	1313	2 US-08-463-911-6	Sequence 6, App1
6	293.5	21.5	4517	4 US-09-140-804-9	Sequence 9, App1
7	273	20.0	3275	4 US-09-370-838-151	Sequence 151, App1
8	264.5	19.3	1333	4 US-09-227-357-51	Sequence 51, App1
9	264.5	19.3	1347	4 US-09-140-804-1	Sequence 1, App1
10	257	18.8	1263	4 US-09-336-536-9	Sequence 9, App1
11	257	18.8	1263	4 US-09-336-536-8	Sequence 8, App1
12	254.5	18.6	1015	3 US-09-188-930-30	Sequence 30, App1

13	252.5	18.5	1001	3 US-09-188-930-218	Sequence 218, App1
14	251	18.4	1728	4 US-09-336-536-2	Sequence 2, App1
15	251	18.4	1338	4 US-09-336-536-1	Sequence 1, App1
16	241	17.6	1839	1 US-08-383-744-1	Sequence 1, App1
17	241	17.6	1839	2 US-08-999-336-1	Sequence 1, App1
18	241	17.6	1839	5 PCT-US96-01427-1	Sequence 1, App1
19	237.5	17.4	2559	4 US-09-118-408-43	Sequence 43, App1
20	237.5	17.4	2559	4 US-09-506-855-43	Sequence 43, App1
21	226	16.5	2769	4 US-09-118-408-1	Sequence 1, App1
22	226	16.5	2769	4 US-09-506-855-1	Sequence 1, App1
23	216.5	15.8	729	4 US-09-140-804-10	Sequence 10, App1
24	203.5	14.9	4359	4 US-09-484-8708-4	Sequence 4, App1
25	200.5	14.7	750	3 US-09-188-930-19	Sequence 19, App1
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27	192	14.0	983	4 US-09-029-348-20	Sequence 20, App1
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38	182	13.3	1703	2 US-08-794-795-1	Sequence 1, App1
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41	179.5	13.1	61663	4 US-07-609-716-62	Sequence 62, App1
42	179.5	13.1	186	1 US-07-609-716-62	Sequence 62, App1
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44	179	13.1	186	1 US-08-642-255-30	Sequence 30, App1
45	179	13.1	186	3 US-08-475-411A-62	Sequence 62, App1

ALIGNMENTS

RESULT 1
US-09-188-930-28
: Sequence 28, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Mathew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James Greg
: TITLE OR INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: and Methods for Their Use
: CURRENT APPLICATION NUMBER: 11000.1011cl
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 28
: LENGTH: 1123
: TYPE: DNA
: ORGANISM: Rat
US-09-188-930-28

Alignment Scores:
Pred. No.: 1,21e-117
Score: 1311.00
Percent Similarity: 97.15%
Best Local Similarity: 95.93%
Query Match: 95.908
DB: 3
Gaps: 0

US-10-036-041-2 (1-246) x US-09-188-930-28 (1-1123)

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DB 180 ATGCTCAGGAGGACGCTGCTGTGCTGACCTGCTGCTTGTCTTCTCCCATTTTGC 239

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Db	240	CTGTCTCAAGTGAATATCATGTGAATCTCCACAACTGGAGGACTCCCCAGACTGCAGC	239
QY	41	LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly	60
Db	300	AAGGTGTGCCATGAGAGATTATGATGATTCCTGGTTACCAAGGCCCCCTGGACCCAGGT	359
QY	61	ProProGlyTLeProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu	80
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US-09-188-930-203			
: Sequence 203, Application US/09188930A			
: Patent NO. 6150502			
: GENERAL INFORMATION:			
: APPLICANT: Watson, James D.			
: APPLICANT: Strachan, Lorna			
: APPLICANT: Sleeman, Matthew			
: APPLICANT: Onrust, Rene			
: APPLICANT: Murison, James Greg			
: TITLE OF INVENTION: Compositions and Methods Isolated From Skin Cells			
: TITLE OF INVENTION: Compositions and Methods For Their Use			
: FILE REFERENCE: 11000.1011c1			
: CURRENT APPLICATION NUMBER: US/09/188,930A			
: CURRENT FILING DATE: 1998-11-09			
: NUMBER OF SEQ ID NOS: 348			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 203			
: LENGTH: 1123			
: TYPE: DNA			
: ORGANISM: Rat			
US-09-188-930-203			
Alignment Scores			

Preid. No.:	1.21e-117	Length:	1123
Score:	1311.00	Matches:	236
Percent Similarity:	97.15%	Conservative:	3
Best Local Similarity:	95.93%	Mismatches:	7
Query Match:	95.90%	Indels:	0
DB:	3	Gaps:	0
US-10-036-041-2 (1-246) x US-09-188-930-203 (1-1123)			
QY	1 MetLeuTrpAtGInLeuIleTyrTrGInLeuLeuAlaLeuPhePheLeuProPheCys	20	
DB	180 ATGCTACAGAGGACGCTCTTGTGGTGGACCTCGTGGCTTTGGCTTTCTCCCAATTTTTC	239	
QY	21 LeuCySGlnAspGluTyrMetGluSerProGlnIhrGlyLeuProProAspCysSer	40	
DB	240 CTGTCTCAAGTATGATACATGGAATCTCCACAACTGGAGGACTGCCCCCAAGACTGCAGC	299	
QY	41 LysCySCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly	60	
DB	300 AAGTGTGTCATGAGATTTATGAGTTCCTGGTGTACCAAGGGCCCCCTGGAGCCCCAGGT	359	
QY	61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlnHisGlu	80	
DB	360 CTTCTGGCATTTCCAGGAACCAATGAAATGAATGAACGAGGACCTGGCCACAGAA	419	
QY	81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyGlyAlaArgGlyGln	100	
DB	420 GGGGCGCAAGGGTGAAGAAAGGAGCAAAAGCGGACCTGGGGCTTCAGGGGCAACGGGGCAG	479	
QY	101 HisGlyProLysGlyGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe	120	
DB	480 CATGGCCCCAAGGATGGAAGGATGCCACAGGGGTGCCACAGAGCTGCAGATTGCCCTTC	539	
QY	121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal	140	
DB	540 ATGGCTTCTACAGGACTCACTTACGAAATCAGAACAGTGGCATTTACTTCACAGACTGT	599	
QY	141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyIleArgPheGlyAlaProValSer	160	
DB	600 GAGACCAACATTTGGAAACTCTTGTGATGTCATGACTGTGATTTGGGGCCCCCGTATCA	659	
QY	161 GlyAlaTyrPhePheThrPheSerMetMetLysHisGlnAspValGluGluValTyrVal	180	
DB	660 GGGCGTATTTCTTCACCTTCAGCATATGACCATGATGAGACCTGGAGGAAGTGTATGTG	719	
QY	181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlnMetLysGlyLys	200	
DB	720 TACCTTATGCAACATGGTGAACACGGTCTTCACGATGTGTAACGATATGAAACAAAGGAAAA	779	
QY	201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrLeu	220	
DB	780 TCACATACATCCACCAACCAATGACGTCTCTAAGTTGGCCAAAGAGATGTGAAGTCTGGCTA	839	
QY	221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnIhrPheSerThrPheAlaGlyPhe	240	
DB	840 AGAATGGCAACGGTGGCCCTTCATGGGGACACCAAGCGCTTCTTACCTTCGACAGGCTTT	899	
QY	241 LeuLeuPheGluThrLys 246		
DB	900 CTCGCTTTTGAACCTAAG 917		
RESULT 3			
US-09-188-930-217			
: Sequence 217, Application US/09188930A			
: Patent No. 6150502			
: GENERAL INFORMATION:			
: APPLICANT: Watson, James D.			
: APPLICANT: Strachan, Lorna			
: APPLICANT: Sleeman, Matthew			
: APPLICANT: Omrust, Rene			
: APPLICANT: Murison, James Greg			
: TITLE OF INVENTION: Compositions Isolated From Skin Cells			
: TITLE OF INVENTION: and Methods For Their Use			


```

Db 160 TGTGCA-----GCTTGATGCA-----GGCATC 183
QY 62 ProglylleProglyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGly 81
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 184 CAGAGATCTCTGCGCAGATGACACAGCGCGATGATGAGATGACATCTCTGCA 243
QY 82 AlAlAsnGlyLysGlyAspLysGlyAspLeuGlyProArgGlyGly 98
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 244 GAGAAAGGAGAAAGAGATGAGCTTCTTGTCTTAAGGTGAGACAGAGATGT 303
QY 99 GylGlnHisGlyProLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 304 GGAATGACAGAGCTGAGAGCCAGGGGCTTCCCGGACCCCTGGCAGAAAGAGAG 363
QY 116 -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPhe 128
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 364 CCTGAGACACCGCTATATGATTCGCTCAGCGTTCAGTGTGGGCGTGGAGACCGCGTC 423
QY 129 SerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 148
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 424 ACTGTTCCCATGTACCCATTCCTTACTAAGATCTTCTACAAACCAAGAAATCATTA 483
QY 149 AspValMetThrGlyArgPheGlyAlaProValSerGlyValGlyPheThrPheSer 168
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 484 GAGGCGACAGCTGCAAGTCTACTGCAACATTCGGGACTTACTACTTCTTACCA 543
QY 169 MetMetLysHisGlyAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThr 188
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 544 ATCAGCGTGAC-----ATGAAAGATGTAGAGGTAGCGCTTCTCAGAAAGAGCAAGGCC 597
QY 189 ValPheSerMetLysSerTyrGluMetLysGlyLysSerAspPheSerSerAsnHisAla 208
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 GTTCTCTTCAACACAGCAGATGACAGAAAGATGTGACAGCGCTGTGCTGTG 657
QY 209 ValLeuLysLeuAlaLysGlyAspGluValTyrPheArgMet---GlyAsnGly----- 225
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 CTCTCATCTGAGAGGAGAGACAGTCTGCTCAGGTGATGGGATGGGAGACCA 717
QY 226 ---AlaLeuHisGlyAspHisGlyAsnArgPheSerThrPheAlaGlyPheLeuPhe 243
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 AATGACTCTATGACAGATACGTCAACGACTTACTGCTTCTTCTCTAC 774
RESULT 5
US-08-463-911-6
; Sequence 6, Application US/08463911
; Patent No. 5869330
; GENERAL INFORMATION:
; APPLICANT: Scherer, Philipp F.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millenia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,911.
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI95-05
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1313 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..804
; US-08-463-911-6

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Alignment Scores:

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Pred. No.: 2,11e-19 Length: 1313
Score: 293.50 Matches: 82
Percent Similarity: 46.47% Conservative: 43
Best Local Similarity: 30.48% Mismatches: 97
Query Match: 21.47% Indels: 48
DB: Gaps: 11

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US-10-036-041-2 (1-246) x US-08-463-911-6 (1-1313)

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QY 9 TrpGlnLeuAlaLeuPheLeuProPhe-----CysLeuGly 23
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 TATCAATTCGCGCTGCGGTTCATTCATACAGAGGCGCTCAGATCTGTCTGG 85
QY 24 AspLysLys-----MetGluSerProGlnThrGly 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 86 GAGCTGTCTACTCTATTAGCTGTCCCGGTACACCAAGAAACAGCTCAAGGCC 145
QY 35 LeuProProAspCysSerLysCysHisGlyAspTyrSerPheArgGlyTyrGlnGly 54
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 ---CCGAGTCTCTCTCCCTGCCCAAGGGG----- 175
QY 55 ProProGlyProProGlyProProGlyIleProGlyAsnHisGlyAsnGlyAsn 74
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 ---CCTCAGAGCTGGATG- GCGGGCATCCAGCGCATCCGCGCATATGAGGCCCA 231
QY 75 GlyAlaThrGlyHisGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 91
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 GCGCGTATGCGCAGATGACACCCCTGGTGAGAGGTGAGAAAGAGATCCAGCTT 291
QY 92 LeuGlyProArg-----GlyGluArgGlyGlnHisGlyProLysGlyLysGly 108
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 ATGCTCTTAAGGAGACATCGTGAACCGAGTACCGCGGCGTGAAGTCCCGAGGC 351
QY 109 TyrProGlyLys-----ProProGlu-----LeuGlnIle 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 352 TTTCGCGGAATCCAAGCAGAGAAAGAGAACTGAGAGGTGCTATGATACCGCTCA 411
QY 119 AlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSer 138
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 GCATTCAGTGTGAGATGAGACTTACGTATGCCCAACATGCCATTCGCTTAC 471
QY 139 SerValGluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaPro 158
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 472 AAGATCTTACAAATCAACAACCACTATGATGCTCCACTGTAATTCACGTGAAC 531
QY 159 ValSerGlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluVal 178
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 532 ATTCCTGGGCTGTACTCTTCCCTACACATCACTAT-----ATGAGAGATGTG 585
QY 179 TyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLys 198
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 586 AAGTCAAGCTCTTCAAGAGAGACAGCTATGCTTCACTATGATCACTACAGAA 645
QY 199 GlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluVal 218
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 AATAATGTGACACGAGCTCCGCTCTGCTCTGATGTGAGGTGGGACCAAGT 705
QY 219 TrpLeuArgMet---GlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPhe 234

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QY	235	SerThrPhealaglyPheLeuLeuPhe 243
Db	706	TGGCTCCAGGCTGTAATGGGGAAGAGAGAGAGATGAGATCTGATGCTGATATGACAAATGAC 7655
QY	235	SerThrPhealaglyPheLeuLeuPhe 243
Db	766	TCCACCTTCACAGAGCTTTCTCTCTAC 792
RESULT 6		
US-09-140-804-9		
Sequence 9, Application US/09140804		
Patent No. 6197930		
GENERAL INFORMATION:		
APPLICANT: Sheppard, Paul O.		
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS		
FILE REFERENCE: 97-49		
CURRENT APPLICATION NUMBER: US/09/140,804		
CURRENT FILING DATE: 1998-08-26		
EARLIER APPLICATION NUMBER: 60/056,983		
EARLIER FILING DATE: 1997-08-26		
NUMBER OF SEQ ID NOS: 47		
SOFTWARE: FastSeq for Windows Version 3.0		
SEQ ID NO 9		
LENGTH: 4517		
TYPE: DNA		
ORGANISM: Homo sapiens		
US-09-140-804-9		
Alignment Scores:		
Pred. No.:	1,14e-18	4517
Score:	293.50	Matches: 83
Percent Similarity:	47.45%	Conservative: 8
Best Local Similarity:	32.55%	Mismatches: 96
Query Match:	21.47%	Indels: 39
DB:	4	Gaps: 11
US-10-036-041-2 (1-246) x US-09-140-804-9 (1-4517)		
QY	9	TrpGlnLeuAlaLeuPhePheLeuProPheCysLeuGlnAsnGlyIuTyMetGlu 28
Db	37	TGGGAGCG-----TTCTACTGGCATTAAGCTCTGCGCGGCG-----ATGACACAG 81
QY	29	SerProGlnThrGlyLeuProProAspCysSerIuScyShiGlyAspTySer 48
Db	82	AAACCCAGACACTCAAGGCG-----CCGAGATCTCGTCCCTGCCCAAGGGG----- 129
QY	49	PheArgGlyTyGlnGlyProProGlyIleProProGlyIleProGlyIleProGlyAsnHis 68
Db	130	-----CTGACAGAGTTGGATG-GGGGGCAATCCAGGGCATCCG 167
QY	69	GlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlnGlyAlaLysGlyGlyIuTyAsp 88
Db	168	GGCCATATATGGGGGCGCCAGCGCGTGAATGGCAGAGATGGCACCCCTGGTGAAGAGGTGAG 227
QY	89	LysGlyIuTy-----LeuGlyProArg-----GlyIuArgGlyGlnHisGly 102
Db	228	AAAGAGATCCAGGCTTATTATGTCCTAAGGAGACATAGGTGAACCGGAGTACCCGGG 287
QY	103	ProLysGlyIuTyGlyTyProGlyIle-----ProProGlu--- 115
Db	288	GCTGAGGTCCTCCAGGCTTCCCGGAGATCCACAGCAGGAAGGAGAACTGGAGAGGT 347
QY	116	-----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsn 132
Db	348	GCCTATGATATCCGCTCAGCATTTAGTGTGGGATTTGCAGACATTACGTTATATATCCCAAC 407
QY	133	SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheValMetThr 152
Db	408	ATGCCCATTCGCTTTACACAGATCTTACATATAGCAAAACCACTATGATGGCTCCACT 467
QY	153	GlyArgPheGlyAlaProValSerGlyValIuTyPhePheThrPheSerMetMetLysHis 172
Db	468	GGTAATATCCATCCACATCTCCGGGCTGCTACTTTGGCTACCAACATACACAGTGTAT 527

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OY      173  GUNSPVALGIUGLUALVYUVALTYRLEUMETHIASNGLYASPHThAlAValLeuysMet 192
Db      528  -----ATGAGAGATGTCGAAGGTACAGCCTTTTAAAGAGACAGAGCTATGCTTTCCACC 581
OY      193  TYTSerTYrIGLumELySGLYsSerASpThSerserASnHISAlAValLeuysleu 212
Db      582  TATGATCAGTACACAGGAATAATATGTAAGACACAGCCTCCGGGCTGTGTGCTCTGCATGTCG 641
OY      213  AAlaYsGLySPGLUALVAlTRLeuAlGmet---GLYASGLY-----AlaLeuHIS 228
Db      642  GAGGTGGCGCACCAAGCTGCTCCAGGTGTATGGAGGAGGAGGAGGCTAATGAGACTTAT 701
OY      229  GLYASpHISGLInATrPheSerThrPheAlaGLYPheLeuLeuPhe 243
Db      702  GCTGATATATGACATACACTCACCCTTCACAGGCTTCTCTCTAC 746

RESULT 7
US-09-370-838-151
Sequence 151, Application US/09370838
Patient No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
EARLIER FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ. ID NOS: 289
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 151
LENGTH: 3275
TYPE: DNA
ORGANISM: Homo sapien
US-09-370-838-151

Alignment Scores:
Pred. No.: 6,96e-17 Length: 3275
Score: 273.00 Matches: 72
Percent Similarity: 47.33% Conservative: 43
Best Local Similarity: 29.63% Mismatches: 90
Query Match: 19.97% Indels: 38
DB: Gaps: 8
US-10-036-041-2 (1-246) x US-09-370-838-151 (1-3275)
OY      34  GLYLeuProProAspCysSerLYsCysSHISGLYASpTYSer----- 48
Db      2064  GGAATCCCT-----TCATAATTTCCAAATGAAATTAATAGCCAGCTGCAGTTCCAA 2111
OY      49  PheArgGLYrIGLInGLYrProPro----- 56
Db      2112  GCTTAGAAGATTTCTGGAGCACCCTTATTTCCCAAGGATAAATTTCCAGCAGTGTATAG 2171
OY      57  -----GLYrProProGLYrProProGLYrLeProGLYASnHISGLYASnASnGLYASn 74
Db      2172  CGAGAGAGGAGACATCTGGTGTCCACAGCAAAATTCAGAGAGCAGGGGTGAGTATTTCTTCT 2233
OY      75  GLYAlaThrGLYHISGLIGLYAlaLYsGLYGLYsGLYASpLYsGLYASpLeuGLYrPro 94
Db      2232  CAGGTGAGGAGCCACAGAA---AGAGACAAACGAAACCTTTAAACAGTGTGACTCTGCACAA 2288
OY      95  ArgGLYGLInATrGLYGLIn-----HISGLYrProLYsGLYGLIn--- 106
Db      2289  GGAAGACTCCCGTACATGACATCCCTGTGGATGTGCCAGTGCACAATTCACAGCCACCATTA 2348
OY      107  -----LYsGLYrTYrProGLYrLeProGLYrLeuGLInLeuGLInLeuAlaPheMetaLaser 123

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Best Local Similarity: 29.51% Mismatches: 98
 Query Match: 19.35% Indels: 75
 DB: 4 Gaps: 10

US-10-036-041-2 (1-246) x US-09-227-357-51 (1-1333)

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OY 14 LeupherleuProPhocysLeucysGlnspsgluYrMetGluSerProgluIthrGly 33
DB 119 CTATATGTTACAGTTTGGCATTGTCGACATGACACACCCGGGTAATCAGTTGAAA 178
OY 34 GlyLeuProPaspCysSerLysCysShisGlyAspTyrSerPheArgGlyTyrGln 53
DB 179 GGAGAGAACTACTCCCGCAGATATATCTGC-----AGCATTCCTGGCTTGGCT 226
OY 54 GlyProPoglyProPoglyProPoglyIleProgluYasnHisGlyYasnHisGlyYasn 73
DB 227 GGACCTCCAGGGCCCCCGAGCAAAATGTTCCCTGGGCCCATGTCGATCGGCTT 286
OY 74 AsnGlyAlaThrGlyHisGlyGlyAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 86
DB 287 CCAGGAAAGAGATGGTAGACGCGAGAAAGAGAAAGGTAAGGAAAGGAAAGGTAAGG 346
OY 87 -----GlyAspLysGlyAspLeuGlyProArg 95
DB 347 TTGAGAGGTAGACTGGACCCCTAGCTTGGCCGGTGAAGAAAGGAGACCAAGAGACT 406
OY 96 GlyLeuArgGlyGlnHisGlyProLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 109
DB 407 GGAGAAAGAAAGAACCATAGACAGAGAGAGAGAAAGAAAGTAAGTGCATTTGGCT 466
OY 110 -----ProgluIleProPro----- 114
DB 467 CCTGACCAAGGAGACGAAATGATNCTMTGGACCGGGGCTCCGAGATTGACAA 526
OY 115 -----GluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsn 130
DB 527 TGTGGAAGACTAGCTGCTAAATCCGCTTTCTGTTGGCATACCAACGATCCAGAA 586
OY 131 GlnAsnSerGlyIleIlePheSerSerVal-GluThrAsnIleGlyAsnPheAspVal 150
DB 587 NAAAGACTACTATATATTAACAAGSTCTCTCCAGGAGGAAAGGACATACCAACCC 646
OY 150 IMetThrGlyArgPheGlyAlaProValSer---GlyValTyrPhePheThrPheSerMet 169
DB 647 TGCACACAGGGAAGT-TCATCTGCTTCCAGGGGATCTAATCTTTCTTAAGATAT 705
OY 169 tMet-----LysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnG 186
DB 706 CACATGGCTAATAAGCAT-----CTGGCAATCGGACTGTCACAAATG 750
OY 186 yasnThrValPheSerMetTyrSerTyrGluMetLys-----GlyLys 200
DB 751 G-----CAATACCGGATTAAGCTTCGACGCCCAACACAGAA 789
OY 200 sSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyr 220
DB 790 CCATCATGTGCTGGGGTCCACAGCATCATCTATCTGACGCCAGAAAGATGAGTGGCT 849
OY 220 uArgMet-----GlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThr 236
DB 850 GGAGATTTTCTTCACAGACCAAGATGGCTCTTCTCAACCCAGGTGGCCAGACAGCTT 909
OY 236 rPheAlaGlyPheLeuLeuPhe 243
DB 910 ATTCCTCGGTTTCTCTTATAC 931

```

RESULT 9

US-09-140-804-1
 ; Sequence 1, Application US/09140804
 ; Patent No. 6197930
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Humes, Jacqueline M.

TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
 FILE REFERENCE: 97-49
 CURRENT APPLICATION NUMBER: US/09/140, 804
 CURRENT FILING DATE: 1998-08-26
 EARLIER APPLICATION NUMBER: 60/056, 983
 EARLIER FILING DATE: 1997-08-26
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 1347
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (198)...(926)
 US-09-140-804-1

Alignment Scores:

Pred. No.: 1,37e-16 Length: 1347
 Score: 264.50 Matches: 74
 Percent Similarity: 48.02% Conservative: 35
 Best Local Similarity: 32.60% Mismatches: 93
 Query Match: 19.35% Indels: 25
 DB: 4 Gaps: 9

US-10-036-041-2 (1-246) x US-09-140-804-1 (1-1347)

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OY 34 GlyLeuProPro---AspCysSerLys-----CysCysHisGlyAspTyrSerPhe 49
DB 240 GGCTGCGCCCGCAGCTGACACCAACAAAGATCCCGACGCTTGGCCCGG-----CNC 290
OY 50 ArgGlyTyrGlnGlyProPoglyProPoglyProPoglyIleProgluYasnHisGly 69
DB 291 CCGGCTTCCAGCACCGCCGCGCACCATGCGACGACGAGGCTTCCGCGCGCATGGC 350
OY 70 AsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlyAlaGlyGlyGlyGlyGlyGly 85
DB 351 CGCGAGCGCGCGAGCGCGCGCGCGCGCTCCGGGAGAGAAAGGAGGCGGAGCGCG 410
OY 86 -----LysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyPro 103
DB 411 GGACTGCGCGGACCTGACAGGAGACCCCGGCGCGAGAGAGCGGAGACCCCGGCGCC 470
OY 104 LysGlyGlyLysGlyTyrProgluIleProPoglyLeuGlnIleAlaPheMetAlaSer 123
DB 471 ACCGGGCTGCGCGGAGAGTCTGCTGCTCCCGCATCCCGCTTCAAGCGCTCC 530
OY 124 LeuAlaThrHisPheSerSerAsnHisSerGlyIleIlePheSerSerValGluThrAsn 143
DB 531 GAGAGCGGGTCCCTCCGCGTGTGACGACCCCTTGCCTTGACCGGCTGCTGTGAAAC 590
OY 144 IleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyr 163
DB 591 GAGCAGGACATTACGACCGCCCTCAACCGCAGTTTACCTGCGAGTGGCTGGGCTAC 650
OY 164 PhePheThrPheSerMetLysHisGluAspValGluGluValTyrValTyr----- 181
DB 651 TACTTCGCCGTC-----CATGCCACCGTCTACCGGCGCAGCTGCAGTTGAT 698
OY 182 LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly----- 199
DB 699 CTGGTGAAAGATGGCAATTCATTCGCTTCTTCCACAGTTT---TTCCGGGGGTCGCC 755
OY 200 LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyr 219
DB 756 AAGCAGCGCTGCTCTCGGGGGGCGCATGTGAGGCTGAGACCTGAGGACCAAGTGTG 815
OY 220 LeuArgMetGlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPheSerThr 236
DB 816 GTGCAAGTGGGTGGTGTCATACATTTGACCATGATGACCATCAAGACAGACAGCAC 875
OY 237 rPheAlaGlyPheLeuLeuPhe 243

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Db      237  ---TCAGGCTCTCTCTCTGACGACACAGATCCCGAGCTGTGTCTCCGGGCGAG--- 290
Qy      48  SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn 67
Db      291  -----CCGGGCTCCCGACACACGACGACGACGACGACGACGACGACGACGACGACGACG 344
Qy      68  HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlnAlaAlaGlyGlyGlyGly 87
Db      345  GAGCGCGGTGATGGCGCGGACGCGGACCGGAGCTCGGGAGAGAGAGAGAGAGAGAGAGAG 404
Qy      88  AsplGlyAsnGlyLeuGlyProArgGlyGlu-----ArgGlyGlnHisGlyProGly 104
Db      405  AGACCGGAGCTACCTGCGGACGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 464
Qy      105  GYGlyGlyGlyTyrProGly-----IleProProGlyLeuGlnIleAlaPheMet 121
Db      465  GGGGCTATCGGGCTCGGGGAGAGCTGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 524
Qy      122  AlaSerLeuAlaThrHisPheSerAsnGlnAsnSerglyIleIlePheSerValGlu 141
Db      525  CGATCAGAGAGCGCGGCTACCTCGCGGACGACACACCCCTTACCGCTTGCAGCGGTGCTG 584
Qy      142  ThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSergly 161
Db      585  CTCGATGAGCAGGACATTCGATGCCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 644
Qy      162  ValTyrPhePheThrPheSerMetMetLeuHisGlnAspValGlnGluValTyrValTyr 181
Db      645  GTCTACTACTTGTGCTGTC-----CATGCCACTGTCTACCGGCGGCGGCGGCGGCGGCT 692
Qy      182  -----LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerglyGlnMetGly 199
Db      693  TTTCGATCTTCAAAATGGCCCAATGCATAGCTCTTCTTCCAGTTT---TTTGGGGGG 749
Qy      200  -----LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlu 217
Db      750  TGGCCAAAGACGACCTGCTCTCTCAGGGGCGTGCATGTGAGGCTAGAACCTGAGGACAG 809
Qy      218  ValTyrPheArgMetGlyAsnGly-----AlaLeuHisGlyAsnHisGlnAlaArgPhe 234
Db      810  GTATGGCTCAGGTGGGTGTGGGTGATTTGATTTGGCATTTATGCCAGCATCAAAACAGAC 869
Qy      235  SerThrPheAlaGlyPheLeuPhe 243
Db      870  AGTACCTTCTCTGATTTCTCTGCTAT 896

RESULT 14
US-09-336-536-2
; Sequence 2, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leibny, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-336-536-2

Alignment Scores:
Pred. No.: 1, 19e-15 Length: 728
Score: 251.00 Matches: 74
Percent Similarity: 48.028 Conservative: 35
Best Local Similarity: 32.608 Mismatches: 93
Query Match: 18, 368 Indels: 26

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DB:      4 Gaps: 9
US-10-036-041-2 (1-246) x US-09-336-536-2 (1-728)
Qy      34  GlyLeuProPro---AspCysSerLys-----CysGlyHisGlyAspTyrSerPhe 49
Db      43  GGCTCGCCCTCCAGTGCAGACACAAAGATCCAGGCTCTGCGCGGG-----CAC 93
Qy      50  ArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsnHisGly 69
Db      94  CCGGCGCTTCCAGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 153
Qy      70  AsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlnAlaAlaGlyGlyGlyGlyGly 86
Db      154  CGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 212
Qy      87  -----GlyAspLysGlyAsnGlyProArgGlyGluArgGlyGlnHisGlyPro 103
Db      213  GACAGTCCCGGAGCTCTGAGGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 272
Qy      104  LysGlyGlyGlyGlyTyrProGlyIleProProGlyLeuGlnIleAlaPheMetAlaSer 123
Db      273  ACCGGGCTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 332
Qy      124  LeuAlaThrHisPheSerAsnGlnAsnSerglyIleIlePheSerValGluThrAsn 143
Db      333  GAGAGCGGCGGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 392
Qy      144  IleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerglyValTyr 163
Db      393  GAGCAGGAGCATACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 452
Qy      164  PhePheThrPheSerMetMetLeuHisGlnAspValGlnGluValTyrValTyr----- 181
Db      453  TACTTGGCGCTC-----CATGCCAGCTTACCGGCGGCGGCGGCGGCGGCGGCTTGT 500
Qy      182  LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerglyGlnMetGly----- 199
Db      501  CTGCTGAAAGATGCGCAATGCATAGCTCTTCTTCCAGTTT---TTGCGGGGGGTGGGCC 557
Qy      200  LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyr 219
Db      558  AACCCAGGCTCTCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 617
Qy      220  LeuArgMetGlyAsnGly-----AlaLeuHisGlyAsnHisGlnAlaArgPheSerThr 236
Db      618  GTCCAGGTGGGTGTGGGTGCTACTATTTGGCATTTATGCCAGCATCAAGACAGACGAC 677
Qy      237  PheAlaGlyPheLeuLeuPhe 243
Db      678  TTCTCCGGATTTCTGCTGTAC 698

RESULT 15
US-09-336-536-1
; Sequence 1, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leibny, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-336-536-1

Alignment Scores:

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Pred. No.: 2,72e-15 Length: 1338
Score: 251.00 Matches: 74
Percent Similarity: 48.02% Conservative: 35
Best Local Similarity: 32.60% Mismatches: 93
Query Match: 18.36% Indels: 26
DB: 4 Gaps: 9

US-10-036-041-2 (1-246) x US-09-336-536-1 (1-1338)

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OY 34 GlyLeuProPro---AspCysSerLys-----CysCysHisGlyAspTyrSerPhe 49
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DB 230 GGCCTGCCCCCTGACGACAAACAGATCCCAAGCTCTGCGCGGGG-----CAC 280
OY 50 ArgGlyTyrGlnGlyProProGlyProProGlyProProGlyLeuProGlyAsnHisGly 69
    ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 281 CCGGCTTCACAGGACCGCGGACCAATGGCCAGGACCAAGGCTTCGCGGCGCGCATGGC 340
OY 70 AsnAsnGlyAsnAsnGlyAlaThrGlyHisGlnGlyAlaLeuGlyGlyLys----- 86
    ::||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 341 CCGGACGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 399
OY 87 -----GlyAspLysGlyAspLeuGlyProArgGlyGlyLeuArgGlyHisGlyPro 103
    ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 400 GCACTGCGCGGACCTCGAGGGAGCCCGCGGCGCGAGAGAGCGGAGCCCGCGGCGCC 459
OY 104 LysGlyGlyLysGlyTyrProGlyLeuProProGlyLeuGlnIleAlaPheMetAlaSer 123
    ||| ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 460 ACCGGGCTGCGGGGAGTCTGCGGCTCGCGCATCCGCTTCAGCGCCAGCGCTCC 519
OY 124 LeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsn 143
    ::||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 520 GAGAGCGCGGCTCGCTCGCGCTGACGACCCCTGCGCGCGCTGCGCGGTGTAAC 579
OY 144 IleGlyAsnPhePheAspValIleThrGlyArgPheGlyAlaProValSerGlyValTyr 163
    ::||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 580 GAGCAGGACATTAACGCGCTCAACCGGCAAGTTCACCTGCCAGGCTCGCGGTCTAC 639
OY 164 PhePheThrPheSerMetMetLysHisGluAspValGluValTyr----- 181
    ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 640 TACTTCGCGCTC-----CATGCCACCGTCTACCGGGGCCAGCCTGCAGTTTGAT 687
OY 182 LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly----- 199
    ||||| ||||| ::||| ||| ::||| ||| ||| ||| ||| ||| ||| ||| |||
DB 688 CTGGTGAAGAATGGCAATCCATGCTCTTCTTCCAGTTT---TTGGGGGGGTGGCCC 744
OY 200 LysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyr 219
    ||| ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 745 AAGCCAGCTCGCTCGCGGGGGGCGCATGTGAGCTGAGGCTGAGGACCAAGTGTGG 804
OY 220 LeuArgMetGlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPheSerThr 236
    ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 805 GTGCAGGTGGGTGTGGTACTACATTTGCAATTCATATGATCCAGCATCAAGACAGACACC 864
OY 237 PheAlaGlyPheLeuLeuPhe 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 865 TTCTCCGGAATTCTGGGTAC 885
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Search completed: January 15, 2003, 21:21:52
Job time : 77 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2003, 19:39:50 ; Search time 3091 Seconds
(Without alignments)
2316.173 Million cell updates/sec

Title: US-10-036-041-2
Sequence score: 1367
Sequence: 1 MLEWOLYQQLALFLFLPFC.....LHGDHQRFTYFAGLLFETK 246

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109380

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O/cgna2_1/USPRO/spool/US10036041/runat_13012003_160808_7058/app.query.fasta.1.391
-DB=GenEmbl -OFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10036041.ecgn.1.1.3637.0runat.13012003.160808.7058 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl: *
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2: gb_htg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
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15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
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33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rtd: *
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41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1367	100.0	1696	6	AX039945	AX039945 Sequence
2	1367	100.0	1709	6	AX136339	AX136339 Sequence
3	1367	100.0	1710	9	AF329837	AF329837 Homo sapi
4	1367	100.0	1730	9	AF326976	AF326976 Homo sapi
5	1311	95.9	1117	6	AX039955	AX039955 Sequence
6	1311	95.9	1879	10	AF246265	AF246265 Mus muscu
7	1291.5	94.5	1927	6	AX191537	AX191537 Sequence
8	1259	92.1	810	6	AX136588	AX136588 Sequence
9	1171	85.7	738	6	AX039954	AX039954 Sequence
10	792.5	58.0	672	6	AX191527	AX191527 Sequence
11	673	49.2	1426	9	BC016021	BC016021 Homo sapi
12	513.5	37.6	546	6	AX079496	AX079496 Sequence
13	315	23.0	912	6	AX054802	AX054802 Sequence
14	315	23.0	1306	9	AF329839	AF329839 Homo sapi
15	315	23.0	3959	9	BC022187	BC022187 Homo sapi
16	315	23.0	3959	9	BC024015	BC024015 Homo sapi
17	313	22.9	1236	10	BC030324	BC030324 Mus muscu
18	309	22.6	1282	6	AX054815	AX054815 Sequence
19	306	22.4	1161	9	AX039965	AX039965 Sequence
20	306	22.4	1176	9	AF329836	AF329836 Homo sapi
21	306	22.4	2404	9	BC011699	BC011699 Homo sapi
22	303	22.2	1134	4	AF269230	AF269230 Bos tauru
23	303	22.2	114675	2	AC010421	AC010421 Homo sapi
24	303	22.2	130630	2	AC010637	AC010637 Homo sapi
25	303	22.2	155013	2	AC026707	AC026707 Homo sapi
26	302.5	22.1	767	10	AY033885	AY033885 Rattus no
27	299	21.9	947	10	BC028770	BC028770 Mus muscu
28	299	21.9	1276	6	AR034252	AR034252 Sequence
29	299	21.9	1276	6	AX195209	AX195209 Sequence
30	299	21.9	1276	6	AX358519	AX358519 Sequence
31	299	21.8	1276	10	MMU37222	U37222 Mus muscu
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35	285.5	21.6	970	10	BC024634	BC024634 Mus muscu
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37	293.5	21.5	734	9	AF404407	AF404407 Macaca mu
38	293.5	21.5	1313	6	AR034253	AR034253 Sequence
39	293.5	21.5	4517	6	AR138194	AR138194 Sequence
40	293.5	21.5	4517	6	AX195211	AX195211 Sequence
41	293.5	21.5	4517	6	AX335029	AX335029 Sequence
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44	293.5	21.5	4545	6	AX134174	AX134174 Sequence
45	293	21.4	1152	6	AX195207	AX195207 Sequence

RESULT 1

ALIGNMENTS

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LOCUS	DEFINITION	Sequence 1 from Patent WO0063377.				
ACCESSION	AX039945					
VERSION	AX039945.1	GI:11229969				
KEYWORDS	SOURCE	human.				
ORGANISM	ORGANISM	Homo sapiens				
REFERENCE	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	AUTHORS	1 (bases 1 to 1696)				
TITLE	TITLE	Piddington, C.S. and Bishop, P.D.				
JOURNAL	JOURNAL	Addpocyte complement related protein homolog zacp3 Patent: WO 0063377-A 1 26-Oct-2000;				
FEATURES	FEATURES	Zymogenetics, Inc. (US)				
SOURCE	SOURCE	Location/Qualifiers				
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		GDVSRFGCGPRGPRGPGIIRGNHNGNNGNNGATHEAKREKDGKGLGRGREGQNG				
		PKGKGTPIGLPELQIAFMASLATHENQNSGATIESSVERINIGFEVMTGRCAVPS				
		GVYEFPTSMKHEDVEEVYVYLMINGNTVPSMSYEMKGRSDTSSNAVLAKAGDEV				
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BASE COUNT	BASE COUNT	482 a 355 c 386 g 473 t				
ORIGIN	ORIGIN					
Alignment Scores:	Alignment Scores:					
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Score:	Score:	1367.00	Matches:	246		
Percent Similarity:	Percent Similarity:	100.00%	Conservative:	0		
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QY	21	LeucysGlnaSpGluTyrMeGluSerProGlnThrglyGlyLeuProProApcysSer	40			
DB	129	CTGTGTCAAGTATGATATGATGAGACTGTCCACAAACCGAGAGACTRACCCCGACTGCAGT	188			
QY	41	LysCysCysHISglYAsPtyrSerPhearglyTyrTrgInglyProProglyProProgly	60			
DB	189	AAGTGTGTCAATGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGCCACCGGGC	248			
QY	61	ProProglyIleProglyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThGlyHisGlu	80			
DB	249	CTCTCTGGCATTTCCAGGAACCATGGAACAAATGGAACCAATGAGAGCCACTGTGATGAA	308			
QY	81	GlyAlaLysGlyGlyLysGlyLysPlyGlyLysPleuglyProArgGlyGlyArgGlyGln	100			
DB	309	GGAGCCAAAGGTGAGAAAGGCGGCAAAAGGTACTCTGGGGCTTCAGGGAGCGGGGGCAG	368			
QY	101	HisGlyProLysGlyGlyLysGlyTyrProglyIleProProglyLueGlnIleAlaPhe	120			
DB	369	CATGGCCCCCAAGAGAGAAAGGCTACCGGGGATTCACACAGAACTTCAGATTCATTC	428			
QY	121	MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal	140			
DB	429	ATGGCTTCTTCGGCAACCCACTTCAGCAATCAGAAACAGTGGATTATCTTCAGCAGTGT	488			
QY	141	GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer	160			
DB	489	GAGACCAACATTTGGAAACCTTTTGATGTCTATGACTGTGATGATTTGGGGCCCAAGTATCA	548			

OY	161	GUYVALTYRPHPEPHEThPhseSerMetWethLyshISgluaSPvalIGluGLValTRVal	180
Dd	549	GCTGTGATTTTCTTCAACCTTCAGCATGATGAAGCATTGGAGATGTGAGAAAGTGATGTG	608
OY	181	TyrlEumetHIsAsnSgLIAsnThVAlPhSeSerMeTyrsErTySGlImetysGIlys	200
Dd	609	TACCTTAGGCACAATGGCACACACTCTTCAGCAGCATGTACAGCTATGAATGAAGGCCAAA	668
OY	201	SerAspThrSerSerAsnHisAlAValLeuLysLeuAlalYSglYaSPclUValTrpleu	220
Dd	669	TCAGATACATCCAGCAACATACGCTCGCTGCAAGCTAACCAAGGGGATGAGCTTGGCTG	728
OY	221	ArgMetGIyaSnGILAlaleuHIsgIlyasrphISgInArGrPheserThrPhAlaGlYphe	240
Dd	729	CGAATGGCCAAATGGCGCTCTCCATGGGACCACCAACCTTCTCCACCTTGGCAGGATTTC	788
OY	241	LeuLeupheGluThrLys	246
Dd	789	CTGCTCTTGAACATAAG	806
RESULT 2			
AXI36339			
LOCUS	AXI36339	1709 bp	DNA
DEFINITION	Sequence 261 from Patent EP1067182.		Linear
ACCESSION	AXI36339		PAT 30-MAY-2001
VERSION	AXI36339.1		
KEYWORDS	GI:14272745		
SOURCE	HUMAN.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1709)		
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.		
TITLE	Secretory protein or membrane protein		
JOURNAL	Patent: EP 1067182-A 261 10-JAN-2001;		
FEATURES	Helix Research Institute (JPI)		
SOURCE	Location/Qualifiers		
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ORIGIN			
Alignment Scores:			
Pred. NO.:	2.44e-96	Length:	1709
Score:	1367.00	Matches:	246
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-10-036-041-2 (1-246) x AXI36339 (1-1709)			
OY	1	MettLeutRpArGlnLeuIlEtYtTpGlnLeuLeuAlalauePhelenuProhEcys	20
Dd	89	ATGCTTTGGAGCGAGCTCATCTATTGGCAACGTGCTGGCTTTGTTTTCCTCCCTTTTTC	148
OY	21	LeucYsgInaspGluTyrmetsLUserProclnhrglgylgauleaupropRoapcysSer	40
Dd	149	CTGTGTCAAGATGATACATGAGAGTCTCCACAAACCGAGAGACTAACCCCAAGACTGCACT	208

OY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
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DB 209 AAGTCTTGTCAATGGAGACTACAGCTTTGAGGCTACCAAGGCCCTCGGGCCACCGGGC 268
OY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGly 80
|||||
DB 269 CCTCTGGCATTCACGAAACCATGGAACATGSCAACATGAGCCACATGCTCATGAA 328
OY 81 GlyAlaIysGlyGlyLeuGlyAspIysGlyAspLeuGlyProArgGlyGlyLeuArgGlyGln 100
|||||
DB 329 GGAGCCAAAGGAGAGAGGCGACAAAGCTGACCTGGGGCCCTCGAGGGGACCGGGGCGAG 388
OY 101 HisGlyProLysGlyGlyLeuLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
|||||
DB 389 CATGGCCCCAAGGAGAGAGGCTTACCCGGGGATTCACCAAGACTTCAGATTCATTC 448
OY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
|||||
DB 449 ATGGCTTCTCGGCAACCCACTTCAGCATGAGACAGTGGGATATATCTTCAGCAGCTT 508
OY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
|||||
DB 509 GAGACCAACATGGAACTCTTTGATGTCATGACTGCTGATTTGGGGCCCACTATCA 568
OY 161 GlyValTyrPhePheThrPheSerMetLysHisGlyAspValGluGlyValTyrVal 180
|||||
DB 569 GGTGTGATTTCTTACCTTCAGCATGATGAGCATGAGATGTTGAGAGACTGATGTG 628
OY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlyLysGlyLys 200
|||||
DB 629 TACCTTATGCAACATGGCAACACAGCTTCACAGCATGTACAGTATGAATGAGGGCAA 688
OY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaIysGlyAspGlyValTyrPhe 220
|||||
DB 689 TCAGATACATCCAGCAATCATCTGTGCTGAGAGCTGAGCAAGGGGATGAGTTGGCTG 748
OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlyAsnArgPheSerThrPheAlaGlyPhe 240
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DB 749 CGAATGGCAATGGGCGCTCTCCATGAGGAGCACCACCAACCTTCCACCTTCAGAGATT 808
OY 241 LeuLeuPheGlyThrLys 246
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DB 809 CTGCTCTTGAACCTAAG 826

RESULT 3
AF329837 1710 bp mRNA linear PRI 12-MAR-2001
LOCUS Homo sapiens complement-clq tumor necrosis factor-related protein
DEFINITION (CTRP3) mRNA, complete cds.
ACCESSION AF329837
VERSION AF329837.1 GI:13274519
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1710)
TITLE Homo sapiens complement-clq tumor necrosis factor-related protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1710)
AUTHORS Piddington, C.S. and Bishop, P.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Ave. East, Seattle, WA 98102, USA
FEATURES
SOURCE
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/map="5p13-p12"
1..1710
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CDS
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84..824
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protein"
/protein_id="AAK1961.1"
/db_xref="GI:13274520"
/translation="MIMROLVYKLLAFPLPELFCODEYMESEPOTGLPPDCSKCH
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PKGERGYPGIPPELQIAFMASLATHSQNSGIIFSVETNIGNFVMTGFGFAPVS
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MLRMNGCALHDHOFSTFAGFLLETK"

BASE COUNT 484 a 358 c 392 g 476 t

ORIGIN

Alignment Scores:
Pred. No.: 2,456-96 Length: 1710
Score: 1367.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-036-041-2 (1-246) x AF329837 (1-1710)

OY 1 MetLeuTyrPArgGlnLeuIleTyrTrpGlnLeuAlaLeuPheLeuProPheCys 20
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DB 84 ATGCTTTGGAGGACCTCTCTATTTGGCAACTGCTGGCTTTTCTCTCTCTCTTTTTC 143
OY 21 LeuCysGlnAspGlyTyrMetGlySerProGlnThrGlyGlyLeuProProAspCysSer 40
|||||
DB 144 CTGTCTCAAGATGATACATGCTGAGCTTCACCAACCGGAGAGACTACCCACAGCTCAGT 203
OY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
|||||
DB 204 AAGCTTTCAGATGAGAGACTACAGCTTTCAGAGCTACCAAGGCCCTCGGGCCACCGGGC 263
OY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGly 80
|||||
DB 264 CCTCTGGCATTCACGAAACCATGGAACAAATGGCAATGGAGCCACTGCTCATGAA 323
OY 81 GlyAlaIysGlyGlyLeuGlyAspIysGlyAspLeuGlyProArgGlyGlyLeuArgGlyGln 100
|||||
DB 324 GGAGCCAAAGGAGAGAGGCGACCAAGCTGACCTGGGGCTCGAGAGGAGCGGGGCGAG 383
OY 101 HisGlyProLysGlyGlyLeuLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
|||||
DB 384 CATGGCCCCAAGGAGAGAGAGGCTACCCGGGGATTCACCAAGAACTTCAGATTGCTTC 443
OY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
|||||
DB 444 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAAACAGTGGGATTTCTTCACCACTGTT 503
OY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
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DB 504 GAGACCAACATGGAACTCTTTGATGTCATGACTGAGTGGATTTGGGGCCCGAGTATCA 563
OY 161 GlyValTyrPhePheThrPheSerMetLysHisGlyAspValGluGlyValTyrVal 180
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DB 564 GGTGTGATTTCTTACCTTCAGCATGATGAGCATGAGAGATGTTGAGGAAGTATGTG 623
OY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlyLysGlyLys 200
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DB 624 TACCTTATGCAACATGGCAACACAGCTTCACCATGTATACAGCTATGAATGAGGGCAA 683
OY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaIysGlyAspGlyValTyrPhe 220
|||||
DB 684 TCAGATACATCCAGCAATATATGCTGTGCTGAACTGACCAAGGGAGATGAGGTTTGCTG 743
OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlyAsnArgPheSerThrPheAlaGlyPhe 240
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DB 744 CGAATGGCAATGGGCGCTCTCCATGAGGAGCACCACCAAGCTTCTCCACCTTCAGAGATT 803

QY 241 LeuLeuphegluThrllys 246
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 Db 804 CTGCTTTGAAACTAG 821

RESULT 4 AF326976

LOCUS AF326976 1730 bp mRNA linear PRI 03-JUL-2001
 DEFINITION Homo sapiens putative secretory protein COR326 mRNA, complete cds.
 ACCESSION AF326976
 VERSION AF326976.1 GI:14586742
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1730)
 AUTHORS Maeda,T., Hayashi,A. and Saito,T.
 TITLE Molecular cloning, chromosomal localization, and genomic structure of the human COR326 gene

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1730)
 AUTHORS Maeda,T.
 TITLE Direct Submission
 JOURNAL Submitted (07-DEC-2000) Department of Radiology and Radiation
 Oncology, Graduate School of Dentistry, Osaka University, 1-8
 Yamadaoka, Suita, Osaka 565-0871, Japan

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 /protein_id="AAK70344.1"
 /db_xref="GI:14586743"
 /translation="MLMRQLIWLALFLPFLCQDEYMESPOGTGSLPPDCSKCH
 GDYSPRGYOGPPGPGPGIPGNHNGNNGATGAGAEKDKDLPRGRGCHG
 PGKEKGPVPELOIAFMASLATHEFNONGSIIFFSVETNIGNFPMVTGREGAPVS
 GYFTFTSMKHEDEVEYVYLMHNGNTVSMYSYEMKSKSDTSSNHAVALKAGDEV
 WLMNGALHGDHQRSTFGFLFEFK"

CDS

BASE COUNT 509 a 358 c 390 g 473 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2.48e-96 Length: 1730
 Score: 1367.00 Matches: 246
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-10-036-041-2 (1-246) x AF326976 (1-1730)

QY 1 MetLeuTrpArgGlnLeuLleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCys 20
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 Db 77 ATGCTTTGGAGGCGCATCTATGTGCAACTGCTGCTTTGTTTCTCTCCCTTTTTC 136
 QY 21 LeuGcGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
 |||||||
 Db 137 CTGTGTCAGATGATGATGAGAGTCTCCACAAACCGAGAGACTACCCCGAGACTGCAGT 196
 QY 41 LysCysGlyHisGlyAspTyrSerPheArgGlyTyrGlnGlnProProGlyProProGly 60
 |||||||
 Db 197 AAGTGTTCATGAGAGCTACAGCTTTTCGAGGCTACCAAGCCGCCCTGTGGCCACCGGGC 256
 QY 61 ProProGlyLleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaTrpGlnGly 80
 |||||||
 Db 257 CCTCTGCGCATTCAGAGAAACCATGGAACAATGCGACAATGAGGCACTGTCATGAA 316

QY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyGlyLysGlyGln 100
 |||||||
 Db 317 GGAGCCCAAGGTGAGAGGGGCGACAAAGTGACCTGGGGCTTCAGAGGCGAGCGCCAG 376
 QY 101 HisGlyProLysGlyGlyLysGlyTyrProGlyLleProProGlyLeuGlnLleAlaPhe 120
 |||||||
 Db 377 CATGGCCCAAGAGAGAGAGAGGCGCTACCCGGGATTCACCAAGAACTTCACATTCGATTC 436
 QY 121 MetaLaserLeuAlaTrpHisPheSerAsnGlnAsnSerGlyLleLlePheSerSerVal 140
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 Db 437 ATGCTCTCTGCGAACCCACTTCAGCAATGAGAACTGATTTATCTTCAGCAGTCTT 496

QY 141 GluThrAsnLleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
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 Db 497 GAGACCAACATTTGAAACTCTTTGATGTCATGACTGTTAATTTGGGGCCCCAGATCA 556
 QY 161 GlyValTyrPhePheTrpPheSerMetLysHisGlyAspValGluGluValTyrVal 180
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 Db 557 GGTTGTATTTCTTCACCTTCATGATGATGAGATGAGATGAGATGATGATGATGATG 616

QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlyMetLysGlyLys 200
 |||||||
 Db 617 TACCTTATGCAATGAGCAACAGTCTTCAGCATGTACACTATGAATGAAAGGCCAAA 676

QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlyValTrpLeu 220
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 Db 677 TCACATACATCCACCAATCATGCTGTGCTGAAGCTAGCCAAAGGGATGAGCTTGGCTG 736

QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
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 Db 737 CGAATGGGCAATGGCGCTCTTCATGGGACCAACACCTTCTCCACCTTTCAGATTC 796

QY 241 LeuLeuphegluThrllys 246
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 Db 797 CTGCTTTGAAACTAG 814

RESULT 5
 AX039955 1117 bp DNA linear PAR 18-NOV-2000
 LOCUS AX039955
 DEFINITION Sequence 11 from Patent WO0063377.
 ACCESSION AX039955
 VERSION AX039955.1 GI:11229976
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1117)
 AUTHORS Piddington,C.S. and Bishop,P.D.
 TITLE Adipocyte complement related protein homolog zacrp3
 JOURNAL Patent: WO 0063377-A 11 26-OCT-2000;
 Zymogenetics, Inc. (US)

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 1. 1117
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 GYFTFTSMKHEDEVEYVYLMHNGNTVSMYSYEMKSKSDTSSNHAVALKAGDEV
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BASE COUNT 284 a 272 c 293 g 268 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3.14e-92 Length: 1117
 Score: 1311.00 Matches: 236
 Percent Similarity: 96.75% Conservative: 2

Best Local Similarity: 95.93% Mismatches: 8
Query Match: 95.90% Indels: 0
DB: 6 Gaps: 0
US-10-036-041-2 (1-246) x AX039955 (1-1117)
QY 1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuAlaLeuPheLeuProPheCys 20
DB 111 ATGCTCGGAGCGCCATGCTGGTGGCACCCTGCTGCTTCTTCCTCCATTTTGC 170
QY 21 LeucGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
DB 171 CTGCTGAACATGATCATGAGACTCTCCACAGCTGAGAGACTCCCGACACTGCAGC 230
QY 41 LysCysGlnHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
DB 231 AAGTGTGCGCATGAGATTTATGATTTCTGTTACCAAGGGCCCCCTGGACCTCCAGGT 290
QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
DB 291 CTTCTGCGCATTCAGAGAAACCATGGAACATGGGAACATGAGCTACTGGCCATGAA 350
QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
DB 351 GGGGCCAAAGGTGAGAAAGAGACAAAGGCCACCTAGGCCCTCGAGAGAAAGGGGGCAG 410
QY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
DB 411 CATGGCCCCAAAGAGAGAAAGGCTACCCAGGGGTGCACAGAACTGCAGATTGCATTC 470
QY 121 MetLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
DB 471 ATGGCTTCTAGCACTCATTGACATCAGAACAGTGGCATATCTTCAGCAGTGT 530
QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
DB 531 GAGGCCAATGGAAGAACTTCTGATGCTCATGCTGGAGAAATTTGGGGCCCCGATATCA 590
QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
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QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
DB 651 TACCTTATGCAACAGGCAACACAGTCTTCAGCATGTATGAAACAAGGAGAAA 710
QY 201 SerAspTrpSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPhe 220
DB 711 TCAGATACATCCACCAACCATGAGTGTGAGATTGGCCAAAGAGATGAGATCTGGCTA 770
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
DB 771 AGATGGGCAACGGTGGCTCCACGGGGACCAACAGCGCTTCTCCACTTCGACGGCTTT 830
QY 241 LeuLeuPheGluThrLys 246
DB 831 CTGCTCTTGAAGCTAAG 848
RESULT 6
LOCUS AF246265 1879 bp mRNA linear ROD 29-JAN-2001
DEFINITION Mus musculus collagenous repeat-containing sequence of 26kDa
ACCESSION AF246265
VERSION AF246265.1 GI:11275676
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1879)
AUTHORS Maeda,T., Abe,M., Kurisu,K., Jikko,A. and Furukawa,S.
TITLE Molecular cloning and characterization of a novel gene, CORNS26,

encoding a putative secretory protein and its possible involvement
in skeletal development
JOURNAL J. Biol. Chem. 276 (5), 3628-3634 (2001)
MEDLINE 21264842
PUBMED 11071891
REFERENCE 2 (bases 1 to 1879)
AUTHORS Maeda,T. and Jikko,A.
TITLE Direct Submission
SUBMITTED (16-MAR-2000) Radiology and Radiation Oncology, Osaka
University School of Dentistry, 1-8 Yamadaoka, Suita, Osaka
565-0871, Japan
FEATURES
source Location/Qualifiers
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/gene="CORNS26"
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/note="putative secretory protein"
/product="collagenous repeat-containing sequence of 26kDa
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BASE COUNT 536 a 409 c 426 g 508 t
ORIGIN
Alignment Scores:
Pred. NO.: 5.49e-92 Length: 1879
Score: 1311.00 Matches: 236
Percent Similarity: 96.75% Conservative: 2
Best Local Similarity: 95.93% Mismatches: 8
Query Match: 95.90% Indels: 0
DB: 10 Gaps: 0
US-10-036-041-2 (1-246) x AF246265 (1-1879)
QY 1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuAlaLeuPheLeuProPheCys 20
DB 100 ATGCTCGGAGCGCCATGCTGGTGGCACCCTGCTGCTTCTTCCTCCATTTTGC 159
QY 21 LeucGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
DB 160 CTGTCTCAGATGATATGATGAGTCTCCACAAAGCTGAGAGGCTCCCGACACTGCAGC 219
QY 41 LysCysGlnHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
DB 220 AAGTGTGCGCATGAGATTTATGATTTCTGTTACCAAGGGCCCCCTGGACCTCCAGGT 279
QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
DB 280 CTTCTGCGCATTCAGAGAAACCATGGAACATGGGAACATGAGCTACTGGCCATGAA 339
QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
DB 340 GGGGCCAAAGGTGAGAAAGAGACAAAGGCCCTAGGCCCTCGAGAGAAAGGGGGCAG 399
QY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
DB 400 CATGGCCCCAAAGAGAGAAAGGCTACCCAGGGGTGCCACAGCACTGCAGATTGCATTC 459
QY 121 MetLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
DB 460 ATGGCTTCTTGAACATCATTGACATCAGAACAGTGGCATATCTTCAGCAGCTTT 519
QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160

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QY	161	GIYVALTYRPhetherPhesermetelutynhiSgiuaspvalglucluvAlTYryAl	180	
Db	580	GGTGTGATTTCTTCACCTTCAGCATGATGAAGACATGAGACGTAGAGAAAGTATGTG	639	
QY	181	TYtleutethiSasnglyAsnthYAlPhesermetTYRserTYglumellSgLyS	200	
Db	640	TACCTTAGCACAAAGCGACACACACTCTTCACACATGTACAGCTATGAAACAAAGGAAAA	699	
QY	201	SerAspTHrserSerAsnHISAlaValleuLYSleuAlaLYSgLYAspCluValrPleu	220	
Db	700	TCAGTACATTCACAGAACCATGACATGCTGCTGAGTGGCCAAAGAGATGAGACTGGGCTA	759	
QY	221	ArgmetGlyAsngLYAlaLeuNHISgLYAspniSglnArgrheserThrPheAlaGlyPhe	240	
Db	760	AGAATGGCCAAAGCGGCTCCACCGGGACACCAACGCGCTTCCTCCACCTTGACAGCTTT	819	
QY	241	LeuLeuphegluThrLys	246	
Db	820	CTGCTCTTTGAAACTAAG	837	
AX191537	AX191537	Sequence 59 from Patent WO0149728.		
DEFINITION	AX191537	AX191537		
ACCESSION	AX191537	AX191537		
VERSION	AX191537.1	GI:15209727		
KEYWORDS	human.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 1927)			
JOURNAL	Kato, S. and Kimura, T.			
FEATURES	Human proteins having hydrophobic domains and dnas encoding these proteins			
source	Patent: WO 0149728-A 59 12-JUL-2001;			
	Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)			
	Location/Qualifiers			
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	/protein_id="CAC51163.1"			
	/db_xref="GI:15209728"			
	/translation="MLWRQLIYWLALLFLPELCODEIWEVSGRTNKVYARIVQSH			
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	DKDGLGPRGEGOHGPRGEGKGYPEIPELDQIAFMAISLATHSNNSGIIFFSVETNIG			
	NFLMS"			
BASE COUNT	550 a	416 c	452 g	509 t
ORIGIN				
Alignment Scores:				
Pred. No.:	1..78e-90	Length:	1927	
Score:	1291.50	Matches:	245	
Percent Similarity:	76.80%	Conservative:	0	
Best Local Similarity:	76.80%	Mismatch:	1	
Query Match:	94.48%	Indels:	74	
DB:	6	Gaps:	1	
US-10-036-041-2 (1-246) x AX191537 (1-1927)				
QY	1	MelleutRPATrgInLeuILeTYTrPclInLeuAlaLeuPhePheLeuProPheCys	20	
Db	89	ATGCTTGAGAGGACACCTCATGATGGCAACGCTTGCTTTTCTCCCTTTTGC	148	
QY	21	LeucYsgInaspGluTYrmetGlu-----	28	
Db	149	CTGTCTCAAGTATGAATACATGAGATGAGCGAGACAACTAATAAGGTGTGCAAGAATA	208	

QY	28	-----	28
Db	209	GTGCAAGCCACCCAGACTGGCCGTAGCGGCTTCAGAGGAGAGAAGTAGAGACGGC	268
	28	-----	28
Db	269	AGCCATCTCTAAACCTGGGACCTGTGATATATAACACTTCTACAGACCTTAAATCCTTGAGA	328
QY	28	-----	28
Db	329	CCAGATGAGCTACCGCACCCGAGTAATGACTACAGCCAGATCACCAATTCCTGGGGC	388
QY	29	---SerProglInthGlyGlyLeuProProAspCysSerIysCysCysHisGlyAspIyr	47
Db	389	CAGTCTCCACAAACCGGAGAGACTTACCCCACTGCACATGATGTTGTCATGAGACACTAC	448
QY	48	SerPheArgGlyTYrGlyGlyIleProProGlyIleProProGlyIleProProGlyIleProGlyAsn	67
Db	449	AGCTTTCGAGGCTACCAAGAGCCCTTGGCCACCGGGCCCTCCGTGGCATTCAGAGAAC	508
QY	68	HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlyGlyGlyAlaGlyAlaGlyIleGlyIleGly	87
Db	509	CATGAAACAATATGCGCAAAATGAGACCCACTGTCATGAAGGAGCCAAAGATGAGAAAGGC	568
QY	88	AspIysGlyAspLeuGlyIleProArgGlyIleLumArgGlyIleHisGlyProGlyGlyIleGlyIleGly	107
Db	569	GACCAAGGTGACTGGGGCTCTGAGGGAGGGGGGCGAGCATGGCCCAAGAGCAAGAG	628
QY	108	GlyTYrProGlyIleProProGlyIleGlyIleAlaPheMetAlaSerLeuAlaThrHis	127
Db	629	GGCTACCGGGGATTCACACGAACTTCAGATTGCATTCATGAGCTTCCTGGCAACCCAC	688
QY	128	PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe	147
Db	689	TTTCACCAATCAGAAACAGTGGGATTATCTTCAGCACTGTTGAGACCACCAATGGAAACTTC	748
QY	148	PheAspValMetThrGlyIleArgPheGlyIleAlaProValSerGlyValTYrPhePheThrPhe	167
Db	749	TT-GATGTCATGACTCGTAGATTGGGGCCACAGATACAGAGTATTATTCTTCACCTTC	807
QY	168	SerMetMetIysHisGlyAspValGluGlyIleValTYrValTYrLeuMetHisAsnGlyAsn	187
Db	808	AGCATGATGAAGCAATGAGAGATTGTGAGCAAGTGATGTGACTTATATCCACATGGCAAC	867
QY	188	ThrValPheSerMetTYrSerTYrGluMetIysGlyIysSerAspThrSerSerHis	207
Db	868	ACAGCTTCAGCATATACGCTATGAATGAAGGGCAATACGATACATCCACGACATATAT	927
QY	208	AlaValIleIysIleAlaIleGlyIysPspIleValTYrPheLeuArgMetGlyAsnGlyAlaLeu	227
Db	928	GCTGTGCTGAGACCTAGCCAAAGGGATAGAGCTTGGCTGCGCAATGGCAATGGCCCTTC	987
QY	228	HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGluIleThrIys	246
Db	988	CATGGGAGACCAACACGCTTCCACCTTTGAGAGATTCCGTCTTGAACACTAG	1044
RESULT 8			
AX136588			
LOCUS	AX136588	810 bp	DNA
DEFINITION	Sequence 510 from Patent EP1067182.		
ACCESSION	AX136588		
VERSION	AX136588.1	GI:14272992	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and		
	Hayashi,K.		
TITLE	Secretory protein or membrane protein		
JOURNAL	Patent: EP 1067182-A 510 10-JAN-2001;		

Helix Research Institute (JP)
Location/Qualifiers
1. .810
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 200 a 201 c 218 g 188 t 3 others
ORIGIN

Alignment Scores:
Pred. No.: 2.22e-88 Length: 810
Score: 1259.00 Matches: 234
Percent Similarity: 97.51% Conservative: 1
Best Local Similarity: 97.10% Mismatches: 6
Query Match: 92.10% Indels: 2
DB: Gaps: 0

US-10-036-041-2 (1-246) x AX136588 (1-810)

OY 1 MetLeuTPaRGSLnLeuILEYTRpgInLeuAlaLeuPheLeuProPheCys 20
DB 89 AAGCTTTGGAGGACCTCATCTATTGGCAAGCTGGCTTGTCTTCCTCCCTTTTTC 148

OY 21 LeuCYSGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
DB 149 CTGTCTCAAGATGAAATACATGAGAGTCTCCACAACCGGAGGACTACCCAGACTGCAGT 208

OY 41 LysCYSCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
DB 209 AAGTGTTCAGTAGAGAGACTACAGCTTTCGAGGCTACCAAGGCCCTCCGCGCCACCGGGC 268

OY 61 ProproGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
DB 269 CCTCTGGCATTCACGAAACCATGGAACAATGGCAACATGGAGCCACTGCTCATGAA 328

OY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
DB 329 GGAGCCAAAGGTGAGAAAGGCCACAAAGGTGACTGGGGCTTCGAGAGGAGCGGGGCGAG 388

OY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
DB 389 CATGGCCCCAAGAGAGAGAGGGGCTACCCGGGATTCACAGAACTTCAGATTGCATTC 448

OY 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
DB 449 ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAAACAGTGGATTATCTTCAGCACTGTT 508

OY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
DB 509 GAGACCAACATTTGGAACCTCTTTGATGTCATGACTGATGATTTGGGGCCCAAGTATCA 568

OY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
DB 569 GGTGGTATTTCTTCACCTTCAGCATGATGAGCATGAGAGATGTTGAGAAAGTATGTG 628

OY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
DB 629 TACCTTATGCAAAATGGCAACACAGCTTCACATGTACAGCTATGAAATGAGGGGCAAA 688

OY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
DB 688 TCAGATACATCCAGCAATATGCTGTGCTGAA-CTAGCCAAANAGGATGAGTTTGGCTG 747

OY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
DB 748 CNAAT-GGCAATGGCGCTTTCATGGGAGCACCAACGCTTTCACCTTTCAGAGATTC 806

OY 241 Leu 241
DB 807 CTG 809

RESULT 9
AX039954
LOCUS AX039954 738 bp DNA linear PAT 18-NOV-2000

Sequence 10 from Patent WO0063377.
ACCESSION AX039954
VERSION AX039954.1 GI:11229975
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .738
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Degenerate nucleotide sequence encoding the
polypeptide of SEQ ID NO:2"
BASE COUNT 130 a 74 c 145 g 99 t 290 others
ORIGIN

Alignment Scores:
Pred. No.: 1.18e-81 Length: 738
Score: 1171.00 Matches: 205
Percent Similarity: 83.33% Conservative: 0
Best Local Similarity: 83.33% Mismatches: 41
Query Match: 85.66% Indels: 0
DB: Gaps: 0

US-10-036-041-2 (1-246) x AX039954 (1-738)

OY 1 MetLeuTPaRGSLnLeuILEYTRpgInLeuAlaLeuPheLeuProPheCys 20
DB 1 AAGTGTTCGAGGACCTCATCTATTGGCAAGCTGGCTTGTCTTCCTCCCTTTTTC 60

OY 21 LeuCYSGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
DB 61 YNTGTGARGATGARTATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 120

OY 41 LysCYSCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
DB 121 AARTGTGTCAGGAGGAGATATATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 180

OY 61 ProproGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
DB 181 CCNCCNGNATHCNCGNAAAYCAAYGNAAYAAAYGNAAYAAAYGNAAYAAAYGNAAY 240

OY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
DB 241 GGNGCNAAGGNGARARAGNGAYAAAGNGAYTNGGNCNNGNGNGARAGNGNGCAR 300

OY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
DB 301 CAYGNGCNAAGGNGARARAGNGATAYCCNCGNATHCNCGNATHCNCGNATHCNCGN 360

OY 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
DB 361 ATGGCMMSNVTTCNCAACCAATTTTYSNAAYCARAAVMSNGNTTATHTTYSNMSGNTN 420

OY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
DB 421 GARACNAATATGAGNAAYTTTGTGATGATGAGTATGAGTATGAGTATGAGTATGAGTAT 480

OY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal 180
DB 481 GGNGTATATTTTTCACCTTCAGCATGATGAGCATGAGATGATGAGATGAGATGAGAT 540

OY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
DB 541 TAYTNAATGCAVAAAYGNAAYACNGTNTTYSNATGAYSNATGAYSNATGAYSNATGAY 600

OY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPleu 220
DB 201 TAYTNAATGCAVAAAYGNAAYACNGTNTTYSNATGAYSNATGAYSNATGAYSNATGAY 600

Db 601 WSNCAVCAVMSWMSNAVCAVCGNGTNTNARTNGCNARGGNGAYGANGCTTGCTN 660

Qy 221 ArgmetGlyasnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
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Db 661 MGNATGGMAAGNAGNGCNYTCAYGAGNAYCAVCAARMGNTTYSNACNTTTCGNGMNTY 720

Qy 241 LeuLeupheGluThrLys 246
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Db 721 YTNMYNTTYYGARACNAAR 738

RESULT 10

AX191527 672 bp DNA linear PAT 15-AUG-2001

LOCUS AX191527

DEFINITION Sequence 49 from Patent WO0149728.

ACCESSION AX191527

VERSION AX191527.1 GI:15209709

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 672)

AUTHORS Kato,S. and Kimura,T.

TITLE Human proteins having hydrophobic domains and dnas encoding these proteins

JOURNAL Patent: WO 0149728-A 49 12-JUL-2001;

PROTEGENE Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)

FEATURES

location/Qualifiers

1..672

Source

1. /organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 185 a 170 c 187 g 130 t

ORIGIN

Alignment Scores:

Pred. No.: 1 38e-52 length: 672

Score: 792.50 Matches: 150

Percent Similarity: 66.96% Conservative: 0

Best Local Similarity: 66.96% Mismatches: 1

Query Match: 57.97% Indels: 74

Gaps: 1

US-10-036-041-2 (1-246) x AX191527 (1-672)

Qy 1 MetLeuTrpArgGlnLeuLeuLeuTrpGlnLeuLeuAlaLeuphePheLeuProPheCys 20
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Db 1 ATGCTTTGGAGCAGCATCTATTTGGCAACTGCTGCTTTCTTCCCTTTTC 60

Qy 21 LeucysGlnAspGluTrpMetGlu----- 28
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Db 61 CTGTGTCMAAGATGATACATGAGGTGAGCGGAGAACTAATAAGTGTGCAAGATA 120

Qy 28 ----- 28

Db 121 GTGCAAAAGCCACGACAGACTGCGCGTCCAGAGAGGAGAAAGTGAGAGCGG 180

Qy 28 ----- 28

Db 181 AGCCATCTTAATACTGGAGCTGTGATATAACACTTCTACAGACTTAATCCCTGAGA 240

Qy 28 ----- 28

Db 241 CCAGATGAGTACCGACCCGAGTAGATGACCTAGCCAGATCACCACATCTCTGGGC 300

Qy 29 ---SerProGlnThrGlyGlyLeuProProAspSerLysCysGlyHisGlyAspTyr 47
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Db 301 CAGCTCCACAAACCGGAGGACTACCCCGACAGCTAGTAGTGTTCATGAGAGACTAC 360

Qy 48 SerPheArgGlyTyrGlnGlyProProGlyProProGlyProGlyLys 67
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Db 361 AGCTTTCAGAGCTACCAAGAGCCCGCTGGGCGACCGGCGCTCTCTGCAATTCAGGAAC 420

Qy 68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyLysGly 87

Db 421 CATGAAACCAATGGCAACAAAGGAGCCACTGTCATGAGAGCCAAAGTGAGAGAGGC 480
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Qy 88 AspLysGlyAsnLeuGlyProArgGlyGlyLysGlyGlnHisGlyProLysGlyLys 107
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Db 481 GACAAGGTGACCTGGGCGCCCGAGGGGAGCGGCGACGACTGCCCCCAAGAGAGAG 540

Qy 108 GlyTyrProGlyLysProProGluLeuGlnLeuAlaPheMetAlaSerLeuAlaThrHis 127
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Db 541 GCGTACCCGGGGATTCACACAGAACTTCAGATTCATTCATGCGCTCTCTGGCAACCCAC 600

Qy 128 PheSerAsnGlnAsnSerGlyLysLeuPheSerValGluThrAsnLysGlyAsnPhe 147
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Db 601 TTCAGCAATCAGAACAGTGGATTATCTTCAGCAGTGTGAGACCACATTGGAATTC 660

Qy 148 PheAspValMet 151
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Db 661 TT-GATGTCATG 671

RESULT 11

BC016021 1426 bp mRNA linear PRI 24-OCT-2001

LOCUS BC016021

DEFINITION Homo sapiens, similar to complement-clq tumor necrosis factor-related protein, likely ortholog of mouse COR526 (collagenous repeat-containing sequence of 26-kDa protein), clone MGC:27511 IMAGE:4720611, mRNA, complete cds.

ACCESSION BC016021

VERSION BC016021.1 GI:16359108

KEYWORDS MGC.

SOURCE

ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1426)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

CONTACT: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAL Plate: 38 Row: P Column: 18.

location/Qualifiers

1..1426

Source

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/db_xref="taxon:9606"

/clone="MGC:27511 IMAGE:4720611"

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/clone_id="NH_MGC_79"

/lab_host="DH10B"

/note="Vector: pDNR-LIB"

138..518

/codon_start=1

/product="Similar to complement-clq tumor necrosis factor-related protein, likely ortholog of mouse COR526 (collagenous repeat-containing sequence of 26-kDa protein)"

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/db_xref="GI:16359109"

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Alignment Scores: 1.02e-15 Length: 912
 Pred. No.: 315.00 Matches: 86
 Score: 41.26% Conservative: 32
 Percent Similarity: 41.26% Mismatches: 96
 Best Local Similarity: 30.07% Indels: 72
 Query Match: 23.04% Gaps: 9
 DB: 6

US-10-036-041-2 (1-246) x AX054802 (1-912)

QY 14 LeuPhePheLeuProPheCysLeuGlnAspGluTyrMetGluSerProGlnThrGly 33
 DB 55 CTTATGTTACAGAGTTTGGTCCAGTGCACAAACCCGGGTAATCATCGTGA 114
 QY 34 GlyLeuProProAspCysSerLysCysGlnHisGlyAspTyrSerPheArgGlyTyrGln 53
 DB 115 GGGAGAACTACTCCCGCAGTATATCTGC-----AGCATTCCTGGCTTGCT 162
 QY 54 GlyProProGlyProProGlyProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsn 73
 DB 163 GGACCTCCAGGGCCCGCTGGAGCAATGGTCCCTGGCCCGCATGGTGCATCGGCTT 222
 QY 74 AsnGlyAlaThrGlyHisGlyGlyAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 88
 DB 223 CCAGGAAGAGATGCTAGACGCGCAGGAAAGAGAAAGTGAAGGAAAGGAACTGCAGGT 282
 QY 88 ----- 88
 DB 283 TTGAGAGTAAGACTGACCGCTAGGCTTGGCCGCTGAGAAAGGCAAGAGAGACT 342
 QY 89 -----LysGlyAspLeuGlyProArgGlyGlyArgGlyGlnHisGlyPro----- 103
 DB 343 GGGAGAAAGAGACCATAGACGAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 402
 QY 104 -----LysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 114
 DB 403 CCTGGAACCAAGGAG 462
 QY 115 -----GluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsn 130
 DB 463 TTGGAAGCATCTGCTCAATCCGCTTTCTGCTTGGCATTCACAAACCACTCCAGAA 522
 QY 131 GlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspVal 150
 DB 523 GAAAGACTACCTATTATATTACAGAGTCCCTTCACAGAGAGAGAGAGAGAGAGAGAG 582
 QY 151 MetThrGlyAlaThrGlyAlaProValSerGlyValTyrPheThrPheSerMetMet 170
 DB 583 GCCACAGGAAAGTTCATCTGCTGCTTCCAGGAGATCTATTCTTCTTATGATATCA 642
 QY 171 -----LysHisGlyAspValGluGlyValTyrLeuMetHisAsnGlyAsn 187
 DB 643 TTGGCTAATTAAGCAT-----CTGGCAATCGGACTGATACCAATGG--- 684
 QY 188 ThrValPheSerMetTyrSerTyrGluMetLys-----GlyLysSer 201
 DB 685 -----CATACCGGATTAAGACCTTCAGCCCAACACAGAGAAACCAT 726
 QY 202 AspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPheArg 221
 DB 727 GATGTGCTTCGGGGTCCACAGTCAATCTATCTCAGCCAGAGATGAAGTCTGGAG 786
 QY 222 Met-----GlyAsnGlyAlaLeuHisGlyAspHisGlnThrPheSerThrPhe 237
 DB 787 ATTTTCTTACAGACAGATGGCTCTTCTCAGACCCAGGTTGGCAGACAGCTTATTC 846
 QY 238 AlaGlyPheLeuLeuPhe 243
 DB 847 TCCGGGTTCTCTTATAC 864

RESULT 14
 AF329839 1306 bp mRNA linear PRI 12-MAR-2001
 LOCUS AF329839

DEFINITION Homo sapiens complement-clq tumor necrosis factor-related protein (CTRP7) mRNA, complete cds.
 ACCESSION AF329839
 VERSION 1
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 Piddington, C.S., Sheppard, P.O., Bishop, P. and Lasser, G.W.
 Home sapiens complement-clq tumor necrosis factor-related protein 2 (bases 1 to 1306)
 Piddington, C.S., Sheppard, P.O., Bishop, P. and Lasser, G.W.
 Direct Submission
 Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /chromosome="4"
 /map="4p15"
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 /note="ZACRP7"
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 /product="complement-clq tumor necrosis factor-related protein"
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 /db_xref="GI:13274524"
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 PPGANGSREPHEPRICLPGRDGRGDKRGEKGEKTRGLNGKTRPLSLACSKQGETGK
 KGPICPEKGEKGTIPGPKGKGDGDEGDEPGLPVCROGSLVLSATSVGLTSTPE
 ERLPIIFPKVLEFNEGEHYNPATGKFIQAFGIIYYSYDITLANKHLAIGLVNNGYRI
 KTFDANTGNHDAVSASTYIYLQPEDEVMLEIFTDQNGLFDPGWADSLFSGFLYVD
 TDYLDISDDEL"
 TDYLDISDDEL"

BASE COUNT 420 a 278 c 310 g 298 t
 ORIGIN

Alignment Scores: 1.49e-15 Length: 1306
 Pred. No.: 315.00 Matches: 86
 Score: 41.26% Conservative: 32
 Percent Similarity: 41.26% Mismatches: 96
 Best Local Similarity: 30.07% Indels: 72
 Query Match: 23.04% Gaps: 9
 DB: 9

US-10-036-041-2 (1-246) x AF329839 (1-1306)

QY 14 LeuPhePheLeuProPheCysLeuGlnAspGluTyrMetGluSerProGlnThrGly 33
 DB 98 CTTATGTTACAGAGTTTGGTCCAGTGCACAAACCCGGGTAATCATCGTGA 157
 QY 34 GlyLeuProProAspCysSerLysCysGlnHisGlyAspTyrSerPheArgGlyTyrGln 53
 DB 115 GGGAGAACTACTCCCGCAGTATATCTGC-----AGCATTCCTGGCTTGCT 205
 QY 54 GlyProProGlyProProGlyProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsn 73
 DB 206 GGACCTCCAGGGCCCGCTGGAGCAATGGTCCCTGGCCCGCATGGTGCATCGGCTT 265
 QY 74 AsnGlyAlaThrGlyHisGlyGlyAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 88
 DB 266 CCAGGAAGAGATGCTAGACGCGCAGGAAAGAGAGAAAGTGAAGGAAAGGAACTGCAGGT 325
 QY 88 ----- 88
 DB 326 TTGAGAGTAAGACTGACCGCTAGGCTTGGCCGCTGAGAAAGGAGAGAGACT 385


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Db 714 GAAGACTACCTATTATTAAACAAAGCTCTTTCACAGGAGAGACACTACACCT 773
QY 151 MetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMet 170
Db 774 GCCACAGGAGAGATTCACTCTGTGCTTCCACGAGATCTATTACTTTCTTATGATATCACA 833
QY 171 -----LysHisGlyAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
Db 834 TTGGCTAATTAACCAT-----CTGCATATCGACTGTACACAAATGGG--- 875
QY 188 ThrValPheSerMetTyrSerTyrGluMetLys-----GlyLysSer 201
Db 876 -----CAATACCGATTAAGACCTTCGACGCCAACACACAGAAACCAT 917
QY 202 AspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPheuArg 221
Db 918 GATGTGGCTTCGGGGTCCACAGTCATCTATCTGCAGCCAGACATGAGTCTGGCTGGAG 977
QY 222 Met-----GlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPhe 237
Db 978 ATTTCTTTCACAGACCAGAAATGGCCTTCTCTCAGACCCAGTTGGCGACACACTTATTC 1037
QY 238 AlaGlyPheLeuPhe 243
Db 1038 TCCGGGTTCTCTTATAC 1055
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(without alignments)
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Title: US-10-036-041-2

Perfect score: 1367

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Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues

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Post-processing: Minimum Match 0%
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-YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1238.5	90.6	1103	14	BM924169	BM924169 AGENCOURT
2	1153	84.3	815	13	B1757458	B1757458 603029396
3	1137.5	83.2	1007	14	B0958105	B0958105 AGENCOURT
4	1093	80.0	724	9	A1956432	A1956432 u177b06.y
5	1065	77.9	636	14	B0637986	B0637986 hdl7a10.y
6	1035	75.7	692	9	A1006567	A1006567 ue14d08.y
7	995.5	72.8	680	9	A1527737	A1527737 u128e09.y
8	994	72.7	631	12	BF788496	BF788496 602114255
9	992	72.6	631	12	BF784596	BF784596 602110304
10	958	70.1	656	10	AM318621	AM318621 un02e01.y
11	953	69.7	635	10	BB572119	BB572119 BB572119
12	934	68.3	703	10	BB649178	BB649178 BB649178
13	909	66.5	662	10	BB610546	BB610546 BB610546
14	820.5	60.0	571	9	A1316916	A1316916 u124c04.y
15	793	58.0	828	12	BG400260	BG400260 602464652
16	764.5	55.9	687	13	B1143591	B1143591 602907423
17	741	54.2	525	12	BF924264	BF924264 MR2-NT013
18	733	53.6	475	9	A1430561	A1430561 md89a11.y
19	727	53.2	553	9	AA821459	AA821459 vs25g06.x
20	721	52.7	413	9	A1892360	A1892360 mm59g11.y
21	717	52.5	413	9	A1325676	A1325676 mm59g11.y
22	715	52.3	412	9	AA068843	AA068843 mm59g11.y
23	689	50.4	508	10	BB867706	BB867706 BB867706
24	677	49.5	762	12	BG201468	BG201468 RST20685
25	677	49.5	770	12	BG195757	BG195757 RST14951
26	677	49.5	773	12	BG204962	BG204962 RST24381
27	672	49.2	776	12	BG186424	BG186424 RST5388.A
28	669	48.9	794	12	BG571867	BG571867 602593213
29	669	48.9	804	12	BG203434	BG203434 RST22817
30	646	47.3	474	9	AA637749	AA637749 vt29c01.x
31	643	47.0	464	10	AA318481	AA318481 um97f05.y
32	639	46.7	803	12	BG228003	BG228003 RST41923
33	633	46.3	780	12	BG199309	BG199309 RST18591
34	629	46.0	355	9	AA334609	AA334609 EST38850
35	629	46.0	577	10	AV597266	AV597266 AV597266
36	620	45.4	536	14	R61190	R61190 ynob010.r1
37	568	41.6	341	9	AA322403	AA322403 EST25036
38	546	39.9	529	9	AA224157	AA224157 zt14f03.x
39	521	38.1	294	9	AA332783	AA332783 EST36794
40	513	37.5	299	12	BG195755	BG195755 RST14949
41	453.5	33.2	610	9	A1317686	A1317686 u122d04.y
42	429.5	31.4	513	12	BG202375	BG202375 RST21732
43	411	30.1	540	13	B1964193	B1964193 i66a10.y
44	411	30.1	555	13	B1964101	B1964101 i66a10.y
45	410	30.0	369	14	W64775	W64775 md89a11.r1

ALIGNMENTS

RESULT 1
BM924169
LOCUS BM924169 1103 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT.6630525 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5760396
5', mRNA sequence.
ACCESSION BM924169
VERSION BM924169.1 GI:19374548
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1103)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

Query Match: 84.35% Indels: 7
 DB: 13 Gaps: 0
 US-10-036-041-2 (1-246) x BT57458 (1-815)

QY 3 TTPARGINLEULEYTRTPGINLEULEALALEUPHELEUPROPHECYSLEUCYS 22
 |||||
 DB 20 TGGAGGAGCTCATCTATTGTGGCAACGCTGCTGTGTCTGCT--CCCTTTTGCTGTGT 77
 |||||

QY 23 GlnAspLeuTyrMetGluSerProGlnThrGlyLeuProProAspCysSerLysCys 42
 |||||
 DB 78 CAGGATGAATATACATGAGGTCTCCACAAACCGAGAGACTACCCCGAGCTGAGTAAGTG- 136
 |||||

QY 43 CysHisGlySprLysPheSerPheMetGlyTyrGlnGlyProProGlyProProGlyProPro 62
 |||||
 DB 137 TGTCAATGGAACACACACTTTCAGAGCTTACCAAGGCCCTGGGCCACCGGGCTCTCT 196
 |||||

QY 63 GlyIleProGlnAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlnHisGlyAla 82
 |||||
 DB 197 GGCATTCTCAGGAACCAATGGAACCAATGGAACCAATGGAACCAATGGAACCAATGGAAC 256
 |||||

QY 83 LysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyLeuArgGlyLysGly 102
 |||||
 DB 257 AAGGTGAGAAAGGCGCAAGAGTGACCTGGGGCTGAGGGGAGGGGCGGCGACCATGGC 316
 |||||

QY 103 ProLysGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPheMetAla 122
 |||||
 DB 317 CCCAAGAGAGAGAGGCTACCGGGGATTCACACAGACTTCAGATTGCAATTCATGCT 376
 |||||

QY 123 SerLeuIleThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThr 142
 |||||
 DB 377 TCTCTGGCAACCCACTTCACCAATCAGAACAGTGGATTCTTCACAGAGTGGAGACC 436
 |||||

QY 143 AsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSerGlyVal 162
 |||||
 DB 437 AACATTGGAACCTCTTGATGTCATGACTGGTGAATTTGGGGCCAGTATCAGTGTG 496
 |||||

QY 163 TyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrValTyrLeu 182
 |||||
 DB 497 TATTCTTCACCTTCACAGATGATGACATGAGATGTTGGAGAGTATGTTACCTT 556
 |||||

QY 183 MetHisAsnGlyAsnThrValPheSerMetLysSerTyrGluMetLysGlyLysSerAsp 202
 |||||
 DB 557 ATGCACATGGCACAACAGCTCTTCAGCATGACGCTGATAATGAAAGGCAATTCAGAT 616
 |||||

QY 203 ThrSerSerAsnHisAlaValLeu-LysLeuAla-LysGlyAspGluValTyrLeuArgm 222
 |||||
 DB 617 ACATCCAGCAATCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
 |||||

QY 222 etGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuL 242
 |||||
 DB 676 TGGCAATGGGCTCTCCATGGGGA-CACCAACGCTTCTCCAC-TTTCGACAGATTCTCTGT 733
 |||||

QY 242 eupheGluThrLys 246
 |||||
 DB 734 CTTTGAACCTAAG 747
 |||||

RESULT 3
 BQ958105 1007 bp mRNA linear EST 21-AUG-2002
 LOCUS BQ958105
 DEFINITION ACENCOURL_10013971 NCI_CGAP_Mam2 Mus musculus cDNA clone
 IMAGE:6486507 5', mRNA sequence.
 ACCESSION BQ958105
 VERSION BQ958105.1 GI:22373583
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1007)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: L14M14030 row: a column: 04
 High quality sequence stop: 622.
 Location/Qualifiers
 1. 1007
 /organism="Mus musculus"
 /strain="FVB/N-3"
 /db_xref="taxon:10090"
 /clone="IMAGE:6486507"
 /clone_lib="NCI_CGAP_Mam2"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

BASE COUNT 253 a 236 c 280 g 231 t 7 others
 ORIGIN

Alignment Scores:
 Pred. No.: 3.65e-101 Length: 1007
 Score: 1137.50 Matches: 216
 Percent Similarity: 87.70% Conservative: 5
 Best Local Similarity: 85.71% Mismatches: 21
 Query Match: 83.21% Indels: 10
 DB: 14 Gaps: 5

US-10-036-041-2 (1-246) x BQ958105 (1-1007)

QY 1 MetLeuTPARGINLEULEIETRTTPGINLEULEALALEUPHELEUPROPHECYS 20
 |||||
 DB 95 ATGCTCGGAGGACGCGCATGCTGTGGCGACCTGCTGCTTGTCTTCTCCATTTTGC 154
 |||||

QY 21 LeucysGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
 |||||
 DB 155 CTGTCTCAAGATGAATATGAGCTCCACAGCTGGAGAGACTGCCCCAGACTGCAGC 214
 |||||

QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
 |||||
 DB 215 AAGTGTCCCATGGAGATTAATGATTTGTGCTTTCACAAAGGCCCTCGAGCTCAGAGT 274
 |||||

QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
 |||||
 DB 275 COTCTGCAATTCAGGAACCATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAG 334
 |||||

QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyLeuArgGlyGln 100
 |||||
 DB 335 GGGGCCAAAGGTGAGAAAGAGAGACAAAGCGCCCTGAGGAGAGAGAGAGAGAGAGAG 394
 |||||

QY 101 HisGlyProLysGlyLysGlyTyrProGlyIleProProGlyLeuGlnIleAlaPhe 120
 |||||
 DB 395 CATGGCCCCAAGAGAGAAAGCTACCCAGGGGTGCCACCAAGCTCAGATTGCAATTC 454
 |||||

QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
 |||||
 DB 455 ATGCTCTCTAGCAACTCATCTTCAGCAATCAGCAATGAGCAATGAGCAATGAGCAATG 514
 |||||

QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
 |||||
 DB 515 GAGACCAACATTGGAACCTTTCATGATGATGAGAGATTTGGGGGCCCGCTATCA 574
 |||||

QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspVal-GluGluValTyrVal 180
 |||||
 DB 575 GGTGTATTCTTCTTCACTTCAGCATGATGATGAACATGAGAGAGAGAGAGAGAGAGTATGT 634
 |||||

QY 180 1TYrLeuMeHisnGlyAsnThrValPheSerMetTySerTyrGluMetLysGly 200
 Db 635 GTACCTTATGCACACGCGACACAGCTTACAGCTATGACAAAGGAAA 694
 QY 200 sSerAspThrSerSerAsnHisAlaValLeuLysLeuAla--LysGlyAspGluValTr 219
 Db 695 ATGAGATACATCCAGACATGACAGTCTGAAGTGGCCAAAGAGAGATGACATGCTG 724
 QY 219 pleuAymMeGlyAsnGlyAlaLeu-----HisGlyAspHisGlnArg--Ph 234
 Db 755 GGCTAG-----AATGGGGCAACGNGTCCCTCCACAGCGAGCCACACGCGCTTCTT 808
 QY 234 eSerThrPheAlaGly---PheLeuLeuPheGlu 244
 Db 809 TCCACCTTTCGACGCGCTTTCCTCTTTTGA 842
 RESULT 4
 A1956432 724 bp mRNA linear EST 20-AUG-1999
 LOCUS ul77b06.y1 Sugano mouse kidney mkoa Mus musculus cDNA clone
 DEFINITION IMAGE:2136563 5' similar to SW:CERL_RAT P98087 CEREBELLIN-LIKE
 GLYCOPROTEIN. ; mRNA sequence.
 A1956432
 A1956432.1 GI:5749141
 EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 724)
 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Stepleos,M., Theising,B., Allen,N., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,T., Cardenas,M., McCann,R.,
 Waterston,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Maria M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through INM; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1001239
 Possible reversed clone: similarity on wrong strand
 Seq primer: custom primer used
 High quality sequence stop: 511.
 Location/Qualifiers
 1..724
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2136563"
 /clone_lib="Sugano mouse kidney mkoa"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: Vector: pME18S-FL3; Site:1: DraIII
 (CACTGTGTG); Site:2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 (ATGCGCCCTTTTCTTTTCTTTT); double-stranded cDNA was
 ligated to a DraIII adaptor (TTTGGCCCTACTGG), digested
 and cloned into distinct draIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTCTCTCTTAAAGAGCTGGC and 3' end
 primer CGACCTCGACGCTCGAGCACA."

BASE COUNT 185 a 187 c 190 g 159 t 3 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.76e-97 Length: 724
 Score: 1093.00 Matches: 196
 Percent Similarity: 94.76% Conservative: 3
 Best Local Similarity: 93.33% Mismatches: 11
 Query Match: 79.96% Indels: 0
 Db: 9 Gaps: 0
 US-10-036-041-2 (1-246) x A1956432 (1-724)
 QY 1 MetLeuTrpArgGlnLeuLeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuPropheCys 20
 Db 95 ATGCTGGAGGAGGACGCGCATCTGTGTGACCTGTCTTCTTCTTCTTCTTCTTCTTCTT 154
 QY 21 LeuCyGlnAspGluTrpMetGluSerProGlnThrGlyLeuPropheAspCysSer 40
 Db 155 CTGTGTCAGATTAATATACATGAGTCTCCCAAGCTGAGAGACTGCCCCAGACTGCAGC 214
 QY 41 LysCyGlnHisGlyAspTyrSerPheAlaGlyTyrGlnGlyProProGlyProProGly 60
 Db 215 AACTGTTCGACATGAGATTAATGATTTCGTGTACCAAGGCCCTCGACCTCCAGGT 274
 QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
 Db 275 CTTCTGCGCATTTCCAGAAACATGGAACATGGAACATGGAACATGGAACATGGAACATGGA 334
 QY 81 GlyAlaLysGlyGlyLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
 Db 335 GGGGCCCAAGGTAGAGAAGAGAGCAAAAGGCGACCTAGGCCCTCGAGAGAGAAAGGGGGCAG 394
 QY 101 HisGlyProLysGlyLysGlyGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
 Db 395 CAGGCCCCCAAGAGAGAGAAAGGCTACCAAGGGGTGCCACCAAGCAGCATTCATTC 454
 QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerVal 140
 Db 455 ATGGCTTCTTACCACTACTCTTACCAATCAGAACAGTGTATCTTCTTCTTCTTCTTCTTCTT 514
 QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
 Db 515 GAGACCAACATTTGAAACTCTTCTGATGCATGATGATGATGATGATGATGATGATGATGATGAT 574
 QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlnAspValGluGluValTyrVal 180
 Db 575 GGTTGTATTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 634
 QY 181 TYrLeuMeHisnGlyAsnThrValPheSerMetTySerTyrGluMetLysGlyLys 200
 Db 635 TACCTTATGCACACGCGACACAGCTTACAGCTATGACAAAGGAAA 694
 QY 201 sSerAspThrSerSerAsnHisAlaValLeu 210
 Db 695 TCAGATACATCCAGACATGAGTGTGCTG 724
 RESULT 5
 B0637986 636 bp mRNA linear EST 15-JUL-2002
 LOCUS hd17a10.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
 DEFINITION Homo sapiens cDNA clone hd17a10 5', mRNA sequence.
 B0637986
 B0637986.1 GI:21762445
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 636)
 Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman
 ,J.W., Bouffard,G., Smith,D. and Peterson,K.
 Expressed sequence tag analysis of human retina for the NEIBank

JOURNAL
COMMENT

Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
 Mol. Vis. 8 (4), (2002) In press
 Contact: Mislav G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 17 row: a column: 10
 Seq primer: M13RPL reverse primer (ABI).
 Location/Qualifiers
 1. .636

FEATURES
source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="h017a10"
 /clone_lib="Human Retina cDNA (Un-normalized, unamplified)
): hd/he"
 /issue_type="Retina"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTCTGATCGCGCGGCC(T)15-3'] EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
 BASE COUNT 155 a 156 c 177 g 148 t
 ORIGIN

Alignment Scores:

Pred. No.: 2.75e-94 Length: 636
 Score: 1065.00 Matches: 189
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 77.91% Indels: 0
 Gaps: 0
 DB: 14

US-10-036-041-2 (1-246) x B0637986 (1-636)

OY 1 MetLeuTPARGlnLeuLleTyrrPrglnLeuAlaLeuPheLeuProPheCys 20
 |||||
 DB 69 ATGCTTGGAGGACCTCATATTGGCAACGCTGCTTTTTCCTCCCTTTTGC 128
 OY 21 LeuCySGlnAspGluTyrrMetGlnSerProGlnrHnGlyLeuProAspCysSer 40
 |||||
 DB 129 CTGTCTCAAGATGATACATGATGAGTCTCCACAACCGGAGGAGTACCCCAAGACTGCTCACT 188
 OY 41 LysCySGlnAspGluTyrrSerPheArgGlyTyrrGlnGlyProProGlyProProGly 60
 |||||
 DB 189 AAGGTGTGATGAGACACTACAGCTTTCGAGGCTACCAAGGCCCTTGCGCCACCGGGGC 248
 OY 61 ProProGlyLleProGlyAsnHnHsGlnAsnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
 |||||
 DB 249 CCTCTGGGATTCACAGAAACCATGGAACATGCAACATGAGACCACTGCTATGAA 308
 OY 81 GlyAlaLysGlyGlnLysGlyAspLysGlyAspLeuGlyProArgGlyGlnGlyGln 100
 |||||
 DB 309 GGAGGCAAGAGGTGAGAGGCGCAAGAGGTGACCTGGGGCTTCGAGGAGGCGGGGCG 368
 OY 101 HnGlyProLysGlyGlnLysGlyTyrrProGlyLleProProGlnLeuGlnLleAlaPhe 120
 |||||
 DB 369 CATGGCCCCAAGAGAGAGAGGCTTACCGGGGATTCACCAAGACTTCAAGATTGCTATTC 428
 OY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyLleLlePheSerVal 140

|||||
 DB 429 ATGCTTCTTGCGACACCTTCAGCAATCAGACAGCTGGATTAATCTTCAGCAGTGT 488
 OY 141 GluThrAsnLleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
 |||||
 DB 489 GAGACCAACATTTGGAACATCTTTTATGATGATGATGATGATGATGATGATGATGATGAT 548
 OY 161 GlyValTyrrPhePheThrPheSerMetLysHisGlnAspValGlnGlnValTyrrVal 180
 |||||
 DB 549 GGTGTGATTTCTTCACCTTCAGCATGATGAGATGAGATGAGATGAGATGAGATGATGATG 608
 OY 181 TyrLeuMetHisAsnGlyAsnThrVal 189
 |||||
 DB 609 TACCTTATGCACAAATGCGACACAGCTC 635

RESULT 6

LOCUS

A1006567 692 bp mRNA linear EST 12-JUN-1998
 uel4d08.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:1480335 5' similar to SW:CERL_RAT P98087 CEREBELLIN-LIKE
 GLYCOPROTEIN ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:928691

Possible reversed clone: similarity on wrong strand
 Seq primer: primer name ambiguous
 High quality sequence stop: 471.
 Location/Qualifiers
 1. .692

FEATURES

source

organism

strain

db_xref

clone

clone_lib

dev_stage

note

site_2

insert

base_count

origin

QY	101	HisGlyProLysGlyGluLysGlyTyrProGlyLeuProProGluLeuGlnIleAlaPhe	120
Db	400	CATGGCCCCAAAGAGAGAAAGCGCTACCGAGGTGCCACAGAACTGCACATTGCCATTC	459
QY	121	MetAlaSerLeuAlaThrHisPheSerAsnIlnAsnSerGlyIleIlePheSerSerVal	140
Db	460	ATGGCTTCTTACGAACTCACTTCAGCAATCAGAACATGGCATTAATCTTACGACGCTT	519
QY	141	GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer	160
Db	520	GAGACCAACATTTGAAACTTCTTGCATGTATATGACTGGGAATTTGGGCCCCGATCA	579
QY	161	GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluVal	178
Db	580	GGTGTGTATTTCTTCACCTTCACATCATGATGACATGACATGAGAGAGAGAGCTG	633
RESULT 12			
LOCUS	BB649178	703 bp.	linear
DEFINITION	BB649178 RIKEN full-length enriched, 16 days embryo	head	Mus
ACCESSION	musculus cDNA clone C130060D14.5		mRNA sequence.
VERSION	BB649178		
KEYWORDS	BB649178.1	GI:16483433	
SOURCE	EST.		
ORGANISM	house mouse.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 703)		
	Atakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishiy,I., Ito,M., Kawai,J., Konno,H., Kouda,M., Koyama,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.		
	RIKEN Mouse ESTs (Atakawa,T., et al. 2001)		
	Unpublished (2001)		
	Contact: Yoshinide Hayashizaki		
	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute		
	The Institute of Physical and Chemical Research (RIKEN)		
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
	Tel: 81-45-503-9222		
	Fax: 81-45-503-9216		
	Email: genome-res@gs.c.riken.go.jp,		
	URL: http://genome.gsc.riken.go.jp/		
	Carninci,P., Shibata,Y., Hayata,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)		
	waghi,K., Fujiyake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed sequencer. Genome Res. 10 (11), 1757-1771 (2000)		
	Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.		
	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)		
	Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.		
	Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)		
	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.		

	FEATURES	mouse tissues.	Location/Qualifiers
	Source		
		1..703	/organism="Mus musculus"
			/strain="C57BL/6J"
			/db_xref="taxon:10090"
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			/tissue_type="head"
			/dev_stage="16 days embryo"
			/lab_host="DHIOB"
			/note="Site_1: Salt; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
			GAGGAGAAGATCCACAGACCCTTTTGTGGTTTTTTTAAVNVN 3'1, cDNA was prepared by using triazole thermo-activated reverse transcriptase and subsequently enriched for full-length by capillary electrophoresis. Second strand cDNA was prepared with the primer adapter of sequence [5']
			GAGGAGAAGATTCCTCGATTATTAATAATTCACCCCCCCC 3'. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I"
BASE COUNT	177 a 183 c 197 g 144 t 2 others		
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Alignment Scores:			
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Score:	934.00	Matches:	171
Percent Similarity:	88.50%	Conservative:	6
Best Local Similarity:	85.50%	Mismatches:	22
Query Match:	68.32%	Indels:	1
DB:	10	Gaps:	0
US-10-036-041-2 (1-246) x BB649178 (1-703)			
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Db 96 ATGCCGGGAGGCAGCGCATCTGGGCGCACCTTGCTTGCCTTTCCTCCCAATTTTGC 155			
OY 21 LeucySGlnAspRgiutYMetGlusEProclInrhrgLyglYleuProProAspcyser 40 CTGTCTCAAAGATGAATATGATGACTTCCAACAACCTGGAGACATCCCCAGACTGCAGC 215			
OY 41 LysCySCysHISgLYASPTyrSerPheArgrLyGrnglyPrroProglyLPProProgly 60 AAGTTTCCCATGCGAGATTAATGATTTCGTGTTCATCCAGAGGGCCCCCTGGACCTCCAGGT 275			
OY 61 ProProgILieProgLyaNHISgLYASNsnsgLYasnaENGlyalathrghLIHSgLU 80 Db 276 CCTCCTGGCATTTCCAGGAACCATGGAACAATGGGAACATGGAGCATTCGGCCATGAA 335			
OY 81 GLyalalySLgLyULySLySLyAsplySLySPleunGIProArgrLyglUargLyGLin 100 Db 336 GGGGCGCAAGCTGAGAAAAGAGACAMAAGCGACCTTAGCCCTTCAGAGGAACGGGGGCGAG 395			
OY 101 HISgLYProLYSGlyULySLyGLTYtyrProgLyleProProgluEngInlaleALphe 120 Db 396 CATGGCCCCAAGGAGAAAGGCTACCCAGGGGGGGGCCACCGAACATGCAATTCATTC 455			
OY 121 MetaIsertLeuaLathrHisPheSerAsngLnasnserGLyllellePheSerSerVal 140 Db 456 ATGGCTTCTTACGACACACTTCAGCAAGATAGAAACAGGGGCATTAATCTTCAGCAGGT 515			
OY 141 GluthrasnllegLYasnPhenAspyALMeThrgrLyArghneGLyalaprovaliser 160 Db 516 GAGAGCAACATTGGAAACTTCTTGATGTCCTGATCGTGGAGATTTGGGGCCCCGATATCA 575			

IMAGE:1920870 5', mRNA sequence.
 AI316916
 VERSION AI316916.1 GI:4032183
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 571)
 REFERENCE 1 Marti, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL: contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:977162
 Seq primer: custom primer used
 High quality sequence stop: 502.
 Location/Qualifiers
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 /strain="C57BL"
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 /clone="IMAGE:1920870"
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 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACCTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer
 [ATGCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor (TTTGGGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACCTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCCTCTTAAAGCTGCG and 3' end primer CGACCTGACGCTGACGACA."
 BASE COUNT 143 a 154 c 156 g 118 t
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 Score: 820.50 Matches: 148
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 Best Local Similarity: 75.51% Mismatches: 7
 Query Match: 60.02% Indels: 39
 DB: Gaps: 1
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 QY 21 LeuGlySlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
 DB 158 CTGCTCAAGATGATACATGAGACTCTCCACAACTGGAGAGACTGCCCCAGACTGCAGC 217
 QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProGlyProGly 60

DB 218 AAGTGTGCCATGAGATTATGATTTCTGTTACCAAGGAGCCCTGACCTCCACT 277
 QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
 DB 278 CTTCTGGCATTTCCAGGAACCATGGAACATGGAACATGAGCTACTGCGCATATA 337
 QY 81 GlyAlaLeuSgGlyGluGlySgGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln 100
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 QY 101 HisGlyProLysGlyGlyGluGlyGlyTyrTrpProGlyIleProProGlyLeuGlnIleAlaIle 120
 DB 398 CATGGCCCAAGAGAGAGAAAGGCTACCCAGGGGTGCCACACAGACTCAATTGCCATTTC 457
 QY 121 MetAlaSerLeuAlaTrpHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
 DB 458 ATGGCTTCTTAGCAACTCAC----- 478
 QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
 DB 478 ----- 478
 QY 161 GlyValTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGlyValTyrVal 180
 DB 479 -----TTTCAGCATGATGAGCATGAGCATGAGCATGAGCATGATGTGTG 520
 QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlu 196
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 ACCESSION BG400260
 VERSION BG400260.1 GI:13293708
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 828)
 REFERENCE 1 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: c9apbs-f@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LICM1331 row: h column: 14
 High quality sequence stop: 740.
 Location/Qualifiers
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and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH/MGC Library."

BASE COUNT 233 a 182 c 190 g 223 t
ORIGIN

Alignment Scores:

Pred. No.:	1.42e-67	Length:	828
Score:	793.00	Matches:	149
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US-10-036-041-2 (1-246) x BG400260 (1-828)

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QY 118 IleAlaPheMetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePhe 137
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QY 138 SerSerValGluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAla 157
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QY 158 ProValSerGlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGln 177
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Db 183 CCAGTATCAGGTGTATTTCTTCACCTTCACATGATGATGATGATGATGATGATGATGATG 242

QY 178 ValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMet 197
    |||||||
Db 243 GTGTATGTGTACTTATGACATGACATGACATGACATGACATGACATGACATGACATGAC 302

QY 198 LysGlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGlu 217
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Db 303 AAGGCCAATATGATATACATCCAGCAATATCCTGCTCTGAGCTAGCCAAAGGGGATGAG 362

QY 218 ValTyrPheArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPhe 237
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Search completed: January 15, 2003, 21:20:27
Job time : 2243 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2003, 19:45:56 (Search time 97 Seconds
(without alignments)
1130.759 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MWMQLIYWLLALFLPFC.....LHGDRHSTFAGFLPETK 246

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Database: Published.Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	100.0	1712	9	US-10-036-041-1
2	1367	100.0	1712	9	US-10-035-855-1
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4	849	62.1	1608	10	US-09-822-849A-359

5	315	23.0	1297	10	US-09-728-952-85	Sequence 85, App1
6	299	21.9	1276	10	US-09-776-976-3	Sequence 3, App1
7	299	21.9	1276	10	US-09-758-055-3	Sequence 3, App1
8	299	21.9	1276	10	US-09-909-547-3	Sequence 3, App1
9	293.5	21.5	4517	10	US-09-776-976-5	Sequence 3, App1
10	293.5	21.5	4517	10	US-09-758-055-5	Sequence 5, App1
11	293.5	21.5	4517	10	US-09-909-547-5	Sequence 5, App1
12	293.5	21.5	4517	10	US-09-964-824A-235	Sequence 235, App
13	293	21.4	1152	10	US-09-776-976-1	Sequence 1, App1
14	293	21.4	1152	10	US-09-758-055-1	Sequence 1, App1
15	293	21.4	1152	10	US-09-909-547-1	Sequence 1, App1
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18	290.5	21.3	3089	9	US-09-989-735-46	Sequence 46, App1
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21	290.5	21.3	3089	9	US-09-990-436-46	Sequence 46, App1
22	290.5	21.3	3089	9	US-09-991-181-46	Sequence 46, App1
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27	290.5	21.3	3089	9	US-10-176-758-61	Sequence 61, App1
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36	290.5	21.3	3089	10	US-09-991-163-46	Sequence 46, App1
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41	289.5	21.2	1169	9	US-09-799-777-112	Sequence 112, App
42	289.5	21.2	1775	9	US-10-098-841-26	Sequence 26, App1
43	276.5	20.2	3226	9	US-09-954-456-725	Sequence 725, App
44	273	20.0	3275	9	US-09-854-133-151	Sequence 151, App
45	273	20.0	3275	10	US-09-738-973-151	Sequence 151, App

ALIGNMENTS

RESULT 1
US-10-036-041-1
Sequence 1, Application US/10036041
Publication No. US20020192751A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C8
CURRENT APPLICATION NUMBER: US/10/036.041
PRIOR FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125826
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/127035
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/127706
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/129122
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/130359
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131272
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/132371
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132379
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/132383
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138166
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908, 827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601

PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 1
LENGTH: 1712
TYPE: DNA
ORGANISM: Homo Sapien
US-10-036-041-1

Alignment Scores:
Pred. No.: 2,46e-117 Length: 1712
Score: 1367.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-036-041-2 (1-246) x US-10-036-041-1 (1-1712)

QY 1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPheLeuProPheCys 20
DB 77 ATCTTTGGAGCCAGCCATCATTTGCAACTGCTGCTTTGTTTCCCTTTTTC 136

QY 21 LeuCyGlnAspGluPyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
DB 137 CTGTGTCAAGATGAATACATGAGTCTCCACAAACGAGGAGCTACCCCGACCTGCAGT 196

QY 41 LysCySCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
DB 197 AAGTGTTCATGAGACATCACTTTCGAGGCTACCAAGGCCCTTGGGCCACCGGCG 256

QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
DB 257 CCTCTGCGCATTCAGAAACCATGGAACATGGAACATGGAAGGAGGAGGAGGAGGAG 316

QY 81 GlyAlaIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 317 GGAGCCAAAGGTGAGAGGCGCAAAAGGTGAGGCTGAGGCGGCTGAGGCGGAGGAG 376

QY 101 HisGlyProLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
DB 377 CATGGCCCAAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 436

QY 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
DB 437 ATGGCTTCTCTGCAACCCACTTCACCAATCAGAACAGTGGATTATCTTCACACAGTGT 496

QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyIArgPheGlyAlaProValSer 160
DB 497 GAGACCAACATTGGAAACTTCTTGTGATGATGATGATGATGATGATGATGATGATGAT 556

PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 1
LENGTH: 1712
TYPE: DNA
ORGANISM: Homo Sapien
US-10-036-342-1

Alignment Scores:
Pred. No.: 2,466-117 Length: 1712
Score: 1367.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-036-041-2 (1-246) x US-10-036-342-1 (1-1712)

QY 1 MetLeuTPraGlnLeuIleTyrrTpgInLeuLeuAlaLeuPheLeuProPheCys 20
|||||
DB 77 ATGCTTTGGAGGAGCTCATCTATTGGCAACGCTGCTTTGTTTCTCCCTTTTGC 136
|||
QY 21 LeuCyGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
|||||

DB 137 CTGTGTCAAGATGAATACATGAGTCTCCACAACCGAGAGCACTACCCACAGCTGCAGT 196
QY 41 LysCySCySHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
|||||
DB 197 AAGGTTCATGAGGAGTACAGCTTTTGAGGCTTACCAAGGCCCTCGGGCCACCGGGCC 256
QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
|||||
DB 257 CCTCTGCGATTCGAGAAACCATGGAACATGGAACATGGAACATGGAACATGGAACATGGA 316
QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLysGlyProArgGlyGluArgGlyGln 100
|||||
DB 317 GGAGCCAAAGGTGAGCAAGGCGACAAAGGTGACCTGGGGCTCGAGGGGCGGGGCGAG 376
QY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluGlnIleAlaPhe 120
DB 377 CATGGCCCCAAAGGAGAGAGGCTTACCGGGGATTCACCGAAGACTTCAGATTGCATTG 436
QY 121 MetaLysLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
|||||
DB 437 ATGGCTTCTCTGCGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGAGCTGT 496
QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160
DB 497 GAGACCAACATGGAAGACTTCTTCATGATGATGATGATGATGATGATGATGATGATGAT 556
QY 161 GlyValIlyrPhePheThrPheSerMetMetLysHisGlyAspValGluGluValIlyrVal 180
DB 557 GGTGTGTATTTCTTCACTTCAGCATGATGAGAGCATGAGAGATGATGAGAGATGATG 616
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlnMetLysGlyLys 200
DB 617 TACCTTATGCAATATGCGCACACAGCTTCACGATTCATACGATTAATAAGGCGCAAA 676
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValIlyrPleu 220
DB 677 TCAGATACATCCAGCAATCATGCTGCTGAGAGCTGAGCCAAAGGAGATGAGTTGGCTG 736
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
DB 737 CGAAATGGGCAATGGCGCTTCATGAGGAGCACCAACGCTTCACCTTTGAGGATTC 796
QY 241 LeuLeuPheGluThrLys 246
DB 797 CTGCTCTTTGAACCTAAG 814

RESULT 4
US-09-822-849A-359
Sequence 359, Application US/09822849A
Patent No. US70020045170A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakr
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 359
LENGTH: 1608
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-849A-359

Alignment Scores:

Pred. No.:	1,39e-69	Length:	1608
Score:	849.00	Matches:	159
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	62.11%	Indels:	0
DB:	10	Gaps:	0

US-10-036-041-2 (1-246) x US-09-822-849A-359 (1-1608)

```
QY 88 AsPlysglyAspleuGlyProArgGlyGluArgGlyGlnHisGlyProLysGlyLys 107
    |||||
DB 2 GACAAAGTCACTCGGGCTCGAGGGAGCGGGGCGCATGCGCCCAAGAGAGAAAG 61

QY 108 GlyTyrProGlyLeuProGlyLeuGlnIleIlePheSerValGluThrAsnIleGlyAsn 127
    |||||
DB 62 GGGTACCCGGGGATTCACAGAACTTCACATTCATCTGCTCTCGGCAACCCAC 121

QY 128 PheSerAsnGlnAsnSerGlyIleIlePheSerValGluThrAsnIleGlyAsn 147
    |||||
DB 122 TTCAGCATCAGAAAGTGGATTCATCTTCAGCAGCTTGAGACCAACATTCGAACTTC 161

QY 148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
    |||||
DB 182 TTTCATGTCATGACGTGATGATTTGGGGCCCGCATCAGCTGTATTTCTTCACCTTC 241

QY 168 SerMetMetLysHisGlnAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
    |||||
DB 242 AGCATATGACATGAGATGAGGATTTGAGAGATGTATCTATCTTATGCAATGGCAAC 301

QY 188 ThrValPheSerMetLysTyrGluMetLysGlyLysSerAspThrSerSerAsnHis 207
    |||||
DB 302 ACGAGTTTCAGCATGTACACCTTGAATGAAGGCCAAATCACAATCATTCCACCAATCAT 361

QY 208 AlaValLeuLysLeuAlaLysGlyAspGluValTyrLeuArgMetGlyAsnGlyAlaLeu 227
    |||||
DB 362 GCGTGTCTCAAGCTACCAAGGGGATGAGGTTGGCTCGCAATGGCAATGGCGCTCTC 421

QY 228 HisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPheGlyThrLys 246
    |||||
DB 422 CATGGGACCAACCAAGCTTCTCCACCTTTCAGAGATTCCTCTTTGAACCTAAG 478
```

RESULT 5

US-09-728-952-85

Sequence 85, Application US/09728952

Patent No. US20020111302A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Wang, Jian-Rui

APPLICANT: Yamazaki, Vicki

APPLICANT: Ujwal, Manusha L.

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20020111302A1el Nucleic Acids and

FILE REFERENCE: Polypeptides

CURRENT APPLICATION NUMBER: US/09/728, 952

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PC-FL-Genes Version 2.0

SEQ ID NO 85

LENGTH: 1297

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (80)..(949)

US-09-728-952-85

Alignment Scores:

Pred. No.:	1,94e-20	Length:	1297
Score:	315.00	Matches:	86
Percent Similarity:	41.26%	Conservative:	32
Best Local Similarity:	30.07%	Mismatches:	96
Query Match:	23.04%	Indels:	72
DB:	10	Gaps:	9

US-10-036-041-2 (1-246) x US-09-728-952-85 (1-1297)

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QY 14 LeuPhePheLeuProPheCysLeuGlyAsnAspGluTyrMetGlySerProGlnThrGly 33
    |||
DB 92 CTCTATGTTCAACATTTTCATTCATTTGTCAGCAGACCAACCCCGGGTAAATCACTGAAA 151

QY 34 GlyLeuProProAspCysSerLysCysCysHisGlyAspTyrPheValGlyTyrGln 53
    |||
DB 152 GGAAGAACTACTCCCGCCAGATATATCTCC-----ACCATTCCTCGCTTCCT 199

QY 54 GlyProProGlyProProGlyProGlyIleProGlyAsnHisGlyAsnGlyAsn 73
    |||||
DB 200 GGACCTCCAGGGCCCCCTGGAGCAATGTTCCCTCGGCCCATGCTCGCATCGCGCTT 259

QY 74 AsnGlyAlaThrGlyHisGlnGlyAlaLysGlyGluLysGlyAsp----- 88
    |||
DB 260 CCAAGAAAGATGTTAGACAGCGCAGAAAGAGAAAGAGTGAAGAAGCACTGCAGGT 319

QY 88 ----- 88
DB 320 TTGAGAGTAAGACTGACCGCTAGCTTCGCCGTGAGAAAGGAGCAAGAGAGACT 379

QY 89 -----LysGlyAspLeuGlyProArgGlyGluArgGlyGlnHisGlyPro----- 103
    |||||
DB 380 GCGAAGAAAGACCAATGAGCAGAGAGAGAAAGAGAAAGAGTGAAGTCCAAATTCGTCT 439

QY 104 -----LysGlyGlyLysGlyTyrProGlyIleProPro----- 114
    |||||
DB 440 CTTGACCAAGAGGAGACAGAGAGAGAAAGAGGAGACCCGGGCTGCGTGAAGTTTCAGA 499

QY 115 -----GluLeuGlnIleAlaPheMetAlaSerLeuAlaThrHisPheSerAsn 130
    |||||
DB 500 TGTGGAAGACTCGTCAATATCCGCTTTCTGTTGGCATCACACCACTTACCCAGAA 559

QY 131 GlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPheAspVal 150
    |||||
DB 560 GAAAGACTACTATTAATTAACAGAGCTCTTCAACAGGAGAGCACTACACCT 619

QY 151 MetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMet 170
    |||||
DB 620 GCCACAGGAAAGTTCATCTGCTTCCAGGAGATCTATTAATTTCTTTATGATATCACA 679

QY 171 -----LysHisGlyAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
    |||||
DB 680 TTGCTAATTAAGCAT-----CTGGCAATTCGAGCTGTACCAATGCG--- 721

QY 188 ThrValPheSerMetLysTyrGluMetLys-----GlyLysSer 201
    |||
DB 722 -----CAATACCGGATTAAGACTTCACAGCCCAACACAGAAACCAT 763

QY 202 AspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrPheArg 221
    |||
DB 764 GATGTGCTTCGGGGTCCACAGATCATCTATCTGAGCAGCAAGATGAAGTCTGGCTGAG 823

QY 222 Met-----GlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPhe 237
    |||
DB 824 ATTTTCTTCACAGACCAAGATGCTCTTCTTCAGACCCAGGTTGGCGAGACACTTATTC 883

QY 238 AlaGlyPheLeuLeuPhe 243
    |||
DB 884 TCCGGGTTCTTTATAC 901
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RESULT 6

US-09-776-976-3

```

; Sequence 3, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76 USA REG
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/7758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 3
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: mus musculus
US-09-776-976-3

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Alignment Scores:
Pred. No.: 5.69e-19 Length: 1276
Score: 299.00 Matches: 82
Percent Similarity: 47.10% Conservative: 40
Best Local Similarity: 31.66% Mismatches: 103
Query Match: 21.87% Indels: 34
DB: 10 Gaps: 9

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US-10-036-041-2 (1-246) x US-09-776-976-3 (1-1276)

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OY 4 ATGGLnLeuIlleTyTrrpLnLeuAlaLeuPhePheProPheCysLeuGln 23
DB 43 AGAGAGCTACTGTGCAAGCTCTCTGTTCTTATCTCTGCC---AGTCATGCCGA 99
OY 24 ASPGLuTyMeIcUSePrroGlnThrGlyGly-----LeuProPaspCysSerLys 41
DB 100 GATGAGCTTACTACACACTAGAGAGCTCCTGCTTGTGCTCCACCAAGGAACT 159
OY 42 CysCysHISgLyAsPrTySerPheArgGlyTyrgLnGlyProProGlyProProGlyPro 61
DB 160 TGTGCA-----GGTGGATGCA-----GGCATC 183
OY 62 ProGlyIlleProGlyAsnHISgLyAsnAsnGlyAsnAsnGlyAlaThrcLysHISgLy 81
DB 184 CAGAGCATCTGGGACACATGACACAGCCGCTGATGAGAGATGCACTCTGGA 243
OY 82 ATAlAsGlyLulysGlyAsPrLysGlyAsPrLeuGlyProArgGlyGluArg----- 98
DB 244 GAGAAAGAGAGAAAGAGATGACAGCTCTCTGCTTGAAGGTGAGACAGAGATGTT 303
OY 99 GlyLInHISgLyProLysGlyLulysGlyTyrgLnGlyProGlyIlleProProGly 115
DB 304 GGAATGACAGAGCTGAGAGGCGGCGCTTCCCGGAGCCCTGGAGAGAGAGAG 363
OY 116 -----LeuGlnIlleAlaPheMetAlaSerLeuAlaThrHisPhe 128
DB 364 CCTGGAAGACCGCTTATATGATGCTCAGCGCTTCAGTGGGGCTGGAGACCGCGTC 423
OY 129 SerAsnGlnAsnSerGlyLleIlePheSerSerValGluThrAsnIlleGlyAsnPhePhe 148
DB 424 ACCTGTTCCCATGTACCATTGCTTACTAGATCTTCTACACCAAGAGATCTTAT 483
OY 149 AspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrgLnPhePheThrPheSer 168
DB 484 GACGCGAGACTGTGCAAGTCTTACTGCAACATTCGCGAGACTACTACTTCTTACAC 543

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OY 169 MetMetLysHISgLyAsPrValGluGlyValTyrgLnLeuMetHisAsnGlyAsnThr 188
DB 544 ATCAGCGGTAC-----ATGAAGATGTGAAAGGTGAGGCTCTTCAAGAGCAAGGCC 597
OY 189 ValPheSerMetLysSerTyrgLwMetLysGlyLysSerAspThrSerSerAsnHISAla 208
DB 598 GTTCTCTTCACCTACGACCAAGATGACGAAAGAAATGTGGACGAGCCCTTGCTGTG 657
OY 209 ValLeuLysLeuAlaLysGlyAsPrLysGlyValTyrgLnArgMet---GlyAsnGly----- 225
DB 658 CTCCTTCATCTGAGGTGGAGACCAAGTGTGGCTCCAGGTATGAGGAGGGGACAC 717
OY 226 ---AlaLeuHISgLyAsPrHISgLnArgPheSerThrPheAlaGlyPheLeuPhe 243
DB 718 AATGCACTGTATGACAGATACGTACACGACGTCTACATTACTGCTTCTCTAC 774

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RESULT 7

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US-09-758-055-3
; Sequence 3, Application US/09758055
; Patent No. US20020058617A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76 USA REG
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 3
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: mus musculus
US-09-758-055-3

```

```

Alignment Scores:
Pred. No.: 5.69e-19 Length: 1276
Score: 299.00 Matches: 82
Percent Similarity: 47.10% Conservative: 40
Best Local Similarity: 31.66% Mismatches: 103
Query Match: 21.87% Indels: 34
DB: 10 Gaps: 9

```

US-10-036-041-2 (1-246) x US-09-758-055-3 (1-1276)

```

OY 4 ATGGLnLeuIlleTyTrrpLnLeuAlaLeuPhePheProPheCysLeuGln 23
DB 43 AGAGATCTACTGTGCAAGCTCTCTGTTCTTATCTCTGCC---ATGTCATGCCGA 99
OY 24 ASPGLuTyMeIcUSePrroGlnThrGlyGly-----LeuProPaspCysSerLys 41
DB 100 GATGAGCTTACTACACTAGAGAGCTCCTGCTTGTGCTCCCTCCACCAAGGAACT 159
OY 42 CysCysHISgLyAsPrTySerPheArgGlyTyrgLnGlyProProGlyProProGlyPro 61
DB 160 TGTGCA-----GGTGGATGCA-----GGCATC 183
OY 62 ProGlyIlleProGlyAsnHISgLyAsnAsnGlyAsnAsnGlyAlaThrcLysHISgLy 81
DB 184 CAGAGCATCTGTGGACACATGACACAGCCGCTGATGAGAGATGSCACTCTGGA 243
OY 82 ATAlAsGlyLulysGlyAsPrLysGlyAsPrLeuGlyProArgGlyGluArg----- 98
DB 244 GAGAAAGAGAGAAAGAGATGACAGCTCTTCTGCTTGAAGGTGAGAGAGAGATGTT 303

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: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO: 5
: LENGTH: 4517
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-776-976-5

Alignment Scores:
Pred. No.: 9,35e-18 Length: 4517
Score: 293.50 Matches: 83
Percent Similarity: 47.45% Conservative: 38
Best Local Similarity: 32.55% Mismatches: 96
Query Match: 21,47% Indels: 39
DB: 10 Gaps: 11

US-10-036-041-2 (1-246) x US-09-776-976-5 (1-4517)

OY 9 TTPGInLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGlu 28
   |||:|||||
Db 37 TGGGAGCTG-----TTCTACTGCTATTAGCTGCCGGGC---ATGACCAGG 81

OY 29 SerProGlnThGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSer 48
   |||:|||||
Db 82 AACCCAGCATCAGGAGG---CCGGAGTCTGCTCCCTCCGCCCAAGGGG----- 129

OY 49 PheArgGlyTyrGlnGlyProProGlyProProGlyTyrProGlyTyrProGlyAsnHis 68
   |||:|||||
Db 130 -----CTGCACAGGTTGGATG-GCGGGCATCCCAAGGCATCCG 167

OY 69 GlyAsnAsnGlyAsnAsnGlyAlaThrGlnHisGlnGlyAlaGlyGlyLysGlyAsp 88
   |||:|||||
Db 168 GGCCTAATATGGGGCCCCCAGGCGGTGATGCGAGATGGACCCCTGGTAGAAGGTTAG 227

OY 89 LysGlyAsp-----LeuGlyProArg-----GlyGluArgGlyGlnHisGly 102
   |||:|||||
Db 228 AAGAGAGATCCAGCTTATTGCTCTTAAGGAGACATCGGTGAACCCGAGTACCCGGG 287

OY 103 ProLysGlyGlnLysGlyTyrProGlyTyr-----ProGlu--- 115
   |||:|||||
Db 288 GGTGAAGTCCCGGCGGCTTCCGGGAATCCAGGACAGGAAGAGAACCTGGAGAGGT 347

OY 116 -----LeuGlnIleAlaPheMetAlaSerIleuAlaThrHisPheSerAsnGlnAsn 132
   |||:|||||
Db 348 GCCTATGATATACCGCTCAGCTCAGTGGATGGAGACTTACGTTACTATCCCAAC 407

OY 133 SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThr 152
   |||:|||||
Db 408 ATGCCCATTCGCTTACCAAGATCTTCAATCAATCAAGAAACCACTATATGCTCCACT 467

OY 153 GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetLysHis 172
   |||:|||||
Db 468 GGTAAATATCACTGCAACATCTCTGGGCTGTACTTCTTCCCTACACATGACTAT 527

OY 173 GlyAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMet 192
   |||:|||||
Db 528 -----ATGAAAGATGTGAAGGTCAAGCTCTCAAGAAAGACAAAGGCTTATCCACC 581

OY 193 TyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeu 212
   |||:|||||
Db 582 TATGATCACTACCAAGAAATATATGTGACCAAGCCTCCGGCTGTGCTCTCCACTG 641

OY 213 AlaLysGlyAspGluValTyrLeuArgMet---GlyAsnGly-----AlaLeuHis 228
   |||:|||||
Db 642 GAGGTGGGCGCAAGATGCTGCTCCAGGTGTATGGGAAGAGAGAGGTATGAGACTAT 701

OY 229 GlyArgHisGlnArgPheSerThrPheAlaGlyPheLeuPhe 243
   |||:|||||
Db 702 GGTGATTAATGACAATGACTCCACCTTCAAGGCTTCTCTCTAC 746

RESULT 10
US-09-758-055-5
: Sequence 5, Application US/09758055
```

```

: Patent No. US20020058617A1
: GENERAL INFORMATION:
: APPLICANT: Fruebis, Joachim
: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: APPLICANT: Bihain, Bernard
: TITLE OF INVENTION: ORG3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76 USA, REG
: CURRENT APPLICATION NUMBER: US/09/758,055
: PRIOR FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/176,228
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/198,087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/299,881
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO: 5
: LENGTH: 4517
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-758-055-5

Alignment Scores:
Pred. No.: 9,35e-18 Length: 4517
Score: 293.50 Matches: 83
Percent Similarity: 47.45% Conservative: 38
Best Local Similarity: 32.55% Mismatches: 96
Query Match: 21,47% Indels: 39
DB: 10 Gaps: 11

US-10-036-041-2 (1-246) x US-09-758-055-5 (1-4517)

OY 9 TTPGInLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGlu 28
   |||:|||||
Db 37 TGGGAGCTG-----TTCTACTGCTATTAGCTGCCGGGC---ATGACCAGG 81

OY 29 SerProGlnThGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSer 48
   |||:|||||
Db 82 AACCCAGCATCAGGAGG---CCGGAGTCTGCTCCCTCCGCCCAAGGGG----- 129

OY 49 PheArgGlyTyrGlnGlyProProGlyProProGlyTyrProGlyTyrProGlyAsnHis 68
   |||:|||||
Db 130 -----CTGCACAGGTTGGATG-GCGGGCATCCCAAGGCATCCG 167

OY 69 GlyAsnAsnGlyAsnAsnGlyAlaThrGlnHisGlnGlyAlaGlyGlyLysGlyAsp 88
   |||:|||||
Db 168 GGCCTAATATGGGGCCCCCAGGCGGTGATGCGAGATGGACCCCTGGTAGAAGGTTAG 227

OY 89 LysGlyAsp-----LeuGlyProArg-----GlyGluArgGlyGlnHisGly 102
   |||:|||||
Db 228 AAGAGAGATCCAGCTTATTGCTCTTAAGGAGACATGCGTGAACCCGAGTACCCGGG 287

OY 103 ProLysGlyGlnLysGlyTyrProGlyTyr-----ProGlu--- 115
   |||:|||||
Db 288 GGTGAAGTCCCGGCGGCTTCCGGGAATCCAGGACATGCGTGAACCCGAGTACCCGGG 347

OY 116 -----LeuGlnIleAlaPheMetAlaSerIleuAlaThrHisPheSerAsnGlnAsn 132
   |||:|||||
Db 348 GCCTATGATATACCGCTCAGCTCAGTGGATGGAGACTTACGTTACTATCCCAAC 407

OY 133 SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThr 152
   |||:|||||
Db 408 ATGCCCATTCGCTTACCAAGATCTTCAATCAATCAAGAAACCACTATATGCTCCACT 467

OY 153 GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetLysHis 172
   |||:|||||
Db 468 GGTAAATATCACTGCAACATCTCTGGGCTGTACTTCTTCCCTACACATGACTAT 527

OY 173 GlyAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMet 192
   |||:|||||
Db 528 -----ATGAAAGATGTGAAGGTCAAGCTCTTCAAGAGACAAAGGCTTATCCACC 581
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Db      82 AACACGACTCAAGGCG---CCGAGTCTGCTCCCTCCCAAGGCGG-----129
QY      49 PheArgGlyTYrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsnHis 68
Db      130 -----CCTGCACAGTGGATG-GCGGGCATCCAGGAGATCCG 167
QY      69 GlysAsnGlnGlyAsnGlnGlyAlaThrGlnHisGlnGlyAlaGlyGlnGlyAsp 88
Db      168 GGCATATATGGGCCCCAGGCGCGTGGATGGCAGATGGCACCCTGGTGAGAGAGGTCAG 227
QY      89 LysGlyAsp-----LeuGlyProArg-----GlyGluArgGlyGlnHisGly 102
Db      228 AAAGAGATCCAGGCTTATGTGCTTAAGGAGACATCGGTAACCGGATACCCGGC 287
QY      103 ProLysGlyGlyGlyTYrProGlyIle-----ProProGlu--- 115
Db      288 GCTGAGAGTCCCGGAGGCTTCCGGGAATCCAGGCGAGAAAGAGAACTGGAGAGGT 347
QY      116 -----LeuGlnIleAlaPheMetAlaSerIleuAlaThrHisPheSerAsnGlnAsn 132
Db      348 GCCATGTATACCGCTACATCACTAGTGGATTGAGACTTACGTATATCCCAAC 407
QY      133 SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPheAspValMetThr 152
Db      408 ATGCCATTCCTTACCAAGATCTTACATACAGCAAAACCACTATGATGGCTCCACT 467
QY      153 GlyArgPheGlyAlaProValSerGlyValTYrPhePheThrPheSerMetGlyHis 172
Db      468 GGTAAATCCCTGCAATTCCTGGGCTGTACTCTTGGCTTCCATCCACATCAGTCTAT 527
QY      173 GlnAspValGlnGluValTYrValTYrLeuMetHisAsnGlyAsnThrValPheSerMet 192
Db      528 -----ArgAAAGATGTAAAGTCAAGCTCTTCAAGAAAGACAGGCTTCCACC 581
QY      193 TyrSerTYrGluMetLysGlyLysSerAspThrSerSerAsnHisAlaValLeuGlyLeu 212
Db      582 TATGATCAGTACAGGAATAATATGTGACCAAGGCTCGGCTGTGCTCTGTCATCTG 641
QY      213 AlaLysGlyAspGluValTYrPheuArgMet---GlyAsnGly-----AlaLeuHis 228
Db      642 GAGGTGGCGGCAAGTGTGGCTCCAGGTGTATGGGGAAGAGAGCGTAATGAGCTCTAT 701
QY      229 GlysAsnHisGlnArgPheSerThrPheAlaGlyPheLeuPhe 243
Db      702 GCTGTAATGACATGACTCCACCTTCACAGGCTTCTTCTCTAC 746

RESULT 13
US-09-776-976-1
; Sequence 1, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Friedb's, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Alpaiah, Bernard
; TITLE OF INVENTION: OB63 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76. USA. REG
; CURRENT APPLICATION NUMBER: US/09/776, 976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758, 055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176, 228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198, 087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299, 881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 1152
; TYPE: DNA

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; ORGANISM: mus musculus
; US-09-776-976-1

Alignment Scores:
Pred. No.: 1,78e-18 Length: 1152
Score: 293.00 Matches: 81
Percent Similarity: 46.54% Conservative: 40
Best Local Similarity: 31.15% Mismatches: 99
Query Match: 21.43% Indels: 40
Db: 10 Gaps: 10

US-10-036-041-2 (1-246) x US-09-776-976-1 (1-1152)
QY      6 LeuIleTYrTrGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuGlyAsnGln 25
Db      20 CTACGTTCAGAGCTCTCTGTTCTCTTAACTCTGCC---AGTCATGCCGAGATGAC 76
QY      26 TYrMetGluSerProGlnThrGlyGly-----LeuProAspCysSerLysCys 43
Db      77 GTTACTACAGACTGAGAGAGCTAGCTCTGCTTGGTCTCTCCACCCAGGAGACTTGGCA 136
QY      44 HisGlyAspTYrSerPheArgGlyTYrGlnGlyProProGlyProProGly 63
Db      137 -----GTTGGATGCA-----GGC 151
QY      64 IleProGlyAsnHisGlyAsnAsnGlyAsnGlnGlyAlaThrGlnHisGlnGlyAlaLys 83
Db      152 ATCCAGGACATTCCTGGCCACATAGGCACACAGCGCGTGAATGGCAGATGGCACTCT 211
QY      84 GlyGlyLysGlyAspLysGlyAsp-----LeuGlyProArgLysGluArg----- 98
Db      212 GGAAGAGAGAGAGAGAGAGAGATTCAGGCTCTTGGTGGCTTAAGGCTGAGACAGAGAT 271
QY      99 ---GlyGlnHisGlyProLysGlyGlyTYrProGlyIleProProGlu----- 115
Db      272 GTTGAATGACAGAGACTGAGGCGCTCGGCGCTTCCGGAAACCTTCGACAGAAAGA 331
QY      116 -----LeuGlnIleAlaPheMetAlaSerIleuAlaThrHis 127
Db      332 GAGCTGGAGAAACCCCTTATGTGTATGCTCAAGCTTCAAGTGGGCTGGAGACCCG 391
QY      128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
Db      392 GTCACGTGCCAATGTACCAATTCGCTTACATAGATGTCTACACAAACAGAAATCAT 451
QY      148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTYrPhePheThrPhe 167
Db      452 TATGACAAACAGCACTGGCAAGTTCTACTGCACACATTCGCGGAGCTTACTACTCTCTAC 511
QY      168 SerMetMetLysHisGlnAspValGlnGluValTYrValTYrLeuMetHisAsnGlyAsn 187
Db      512 CACATCAGCGGTAC-----ATGAAAGATGTAAAGTGAAGCTTCAAGAAAGACAG 565
QY      188 ThrValPheSerMetLysGlyGluMetLysGlyLysSerAspThrSerSerAsnHis 207
Db      566 GCCGTCTCTTCACTACAGCAGCAGTACAGAAATAATGTGACCAAGGCTCTGGCTG 625
QY      208 AlaValLeuLysLeuAlaLysGlyAspGluValTYrPheuArgMet---GlyAsnGly--- 225
Db      626 GTGCTCTTCATCTGAGAGTGGGAGACCAAGTCTGCTCAGGTGTATGGGAGTGGGAG 685
QY      226 -----AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuPhe 243
Db      686 CACATGAGCTTATGCAGATACGTAACAGACTTACATTAAGCTTCTCTCTCTC 745

RESULT 14
US-09-758-055-1
; Sequence 1, Application US/09758055
; Patent No. US20020058617A1
; GENERAL INFORMATION:
; APPLICANT: Friedb's, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances

```



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Oy 116 -----LeuGlnIleAlaPheMetAlaSerLeuAlaThrHis 127
Db 332 GAGCCTGGAGAAAGCCGCTTATGCTGATCGCTCAGGCTTCAAGTGGGGCTGGAGACCCGC 391
Oy 128 PheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhe 147
Db 392 GTCACTGTCCCATGTACCATGTACCATGTACCATGTACCATGTACCATGTACCATGTAC 451
Oy 148 PheAspValMetThrGlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPhe 167
Db 452 TATGACAACAGCAGCAGTGGCAAGTTCCTACTGCAACATTCGCGGACTCTACTACTCTTAC 511
Oy 168 SerMetMetLysHisGlnAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsn 187
Db 512 CACATCAGCGGTGAC-----ATGAAAGATGTGAAGGTGAGGCTCTTCAAGAGACAAAG 565
Oy 188 ThrValPheSerMetLysSerTyrGluMetLysGlyLysSerAspPheSerSerAsnHis 207
Db 566 GCCGTTCTCTTCACTACCTACGACACAGTATCAGAAAGATGTGAGCAGGCTCTGCTCT 625
Oy 208 AlaValLeuLysLeuAlaLysGlyAspGluValTyrPheArgMet--GlyAsnGly--- 225
Db 626 GTGCTCTCTCATCTGAGAGGTGAGACCAAGCTGCTGCTCAGGTATGAGGATGGGAGAC 685
Oy 226 -----AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
Db 686 CACAATGAGACTTATGACATTAACGTCAAGACTTACATTACTGCGTTCTTCTCTTC 745
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Search completed: January 15, 2003, 21:23:46
Job time : 106 secs

23-MAR-1999: 99US-0125774.
23-MAR-1999: 99US-0125778.
24-MAR-1999: 99US-0125826.
31-MAR-1999: 99US-0127035.
05-APR-1999: 99US-0127706.
21-APR-1999: 99US-0130359.
27-APR-1999: 99US-0131270.
27-APR-1999: 99US-0131272.
27-APR-1999: 99US-0131291.
04-MAY-1999: 99US-0132371.
04-MAY-1999: 99US-0132379.
04-MAY-1999: 99US-0132383.
25-MAY-1999: 99US-0135750.
08-JUN-1999: 99US-0138166.
20-JUL-1999: 99US-0144791.
03-AUG-1999: 99US-0146970.
09-DEC-1999: 99US-0170262.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2000-628263/60.
DR P-PSDB: AAB18909.
XX
PT Novel secreted and transmembrane polypeptides useful for diagnosing
PT tumour in a mammal, for identifying agonists and antagonists of the
PT polypeptide and for therapeutic use
XX
PS Claim 2: Fig 1; 222pp; English.
XX
CC The present sequence encodes a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5337, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells
CC and are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger's disease or other
CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing.
XX
SQ Sequence 1712 BP; 491 A; 358 C; 388 G; 475 T; 0 other:
Query Match 99.9%; Score 1710.4; DB 21; Length 1712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GGCATCTGCCGAGAGACACACGCTCTGAGAGCTGCTGCTTCTTCAGGAGACTCTGA 60
DB 1 GGCATCTGCCGAGAGACACACGCTCTGAGAGCTGCTGCTTCTTCAGGAGACTCTGA 60
OY 61 GGCCTGTGTGAATCAATGCTTTGGAGGACACTATCTATTGGCAACTGCTGGCTTTGT 120
DB 61 GGCCTGTGTGAATCAATGCTTTGGAGGACACTATCTATTGGCAACTGCTGGCTTTGT 120
OY 121 TTTCCTCCCTTTTGGCTGTGTCAAGATGAATACATGAGAGTCTCCACAACCGAGAGACT 180
DB 121 TTTCCTCCCTTTTGGCTGTGTCAAGATGAATACATGAGAGTCTCCACAACCGAGAGACT 180
OY 181 ACCCCCAACATGCTAGTGTGTGATGAGAGACTACAGCTTTTGGAGGCTACCAAGGCC 240
DB 181 ACCCCCAACATGCTAGTGTGTGATGAGAGACTACAGCTTTTGGAGGCTACCAAGGCC 240
OY 241 CCTGGGCGACCGGGCCTCTGCGATTCAGGAACCATGGAACATGCGACCAATG 300

|||||
DB 241 CCTGGGCGACCGGGCCTCTGCGATTCAGGAACCATGGAACATGCGACCAATG 300
OY 301 AGCCACTGTGTCATGAGAGGCCAAGAGTGAGAGGGGACAAAGAGTGAACCTGGGCTTCG 360
DB 301 AGCCACTGTGTCATGAGAGGCCAAGAGTGAGAGGGGACAAAGAGTGAACCTGGGCTTCG 360
OY 361 AGGGGACCGGGGCGACATGGCCCCCAAGGAGAGAGAGGGCTACCCGGGGATTCCACCGA 420
DB 361 AGGGGACCGGGGCGACATGGCCCCCAAGGAGAGAGAGGGCTACCCGGGGATTCCACCGA 420
OY 421 ACTTCAGATTTCATTCATGCTCTCTGCAACCCACTTCAGCATTCAGAACAGTGGGAT 480
DB 421 ACTTCAGATTTCATTCATGCTCTCTGCAACCCACTTCAGCATTCAGAACAGTGGGAT 480
OY 481 TATCTTCAGCAGTGTGAGACCAACATGGAACCTCTTGTGATGTCATGACTGTAGATT 540
DB 481 TATCTTCAGCAGTGTGAGACCAACATGGAACCTCTTGTGATGTCATGACTGTAGATT 540
OY 541 TGGGGCCCCAGTATCAGGTGTGTATTCTTCACCTTCAGCATGATGAGAGCATGAGATGT 600
DB 541 TGGGGCCCCAGTATCAGGTGTGTATTCTTCACCTTCAGCATGATGAGAGCATGAGATGT 600
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DB 601 TGAGGAGTGTATGTATCTTATGCAACATGGGACAGAGCTTCAGCATGTACAGCTA 660
OY 661 TGAATGAGAGGCAATCAGATACATCCAGCATCATCTGCTGTGAGAGCTACCAAGG 720
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OY 721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCATGGGACACCAACGCTTCTC 780
DB 721 GGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCATGGGACACCAACGCTTCTC 780
OY 781 CACCTTGGCAGAGTTCCTGCTTGTGAACATGATGATATGATGATGATGATGATGATG 840
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OY 841 TTTGGGGAAGACTGTAGCTAGCTGATTTGTAGCATCTGAGGAACATTAAGTTGAGG 900
DB 841 TTTGGGGAAGACTGTAGCTAGCTGATTTGTAGCATCTGAGGAACATTAAGTTGAGG 900
OY 901 GTTTTACATCTGCTGATTCACAAAATTTATGTTGCAATGTTGTTGACGTACAGCTACA 960
DB 901 GTTTTACATCTGCTGATTCACAAAATTTATGTTGCAATGTTGTTGACGTACAGCTACA 960
OY 961 CCAATTAATGTTGCAATTAAGGAGGCTCAGAAAGATCAACCAAAATATGTTCTCAGA 1020
DB 961 CCAATTAATGTTGCAATTAAGGAGGCTCAGAAAGATCAACCAAAATATGTTCTCAGA 1020
OY 1021 TGACCTTGACATAATATACATGACATCTTATCCTCTTGGCACCCTAAAGATAT 1080
DB 1021 TGACCTTGACATAATATACATGACATCTTATCCTCTTGGCACCCTAAAGATAT 1080
OY 1081 TCTCTCTGAGGAGGTTGGAATATTTTCTATACAGAAAGTCATTTGCAAGAAAT 1140
DB 1081 TCTCTCTGAGGAGGTTGGAATATTTTCTATACAGAAAGTCATTTGCAAGAAAT 1140
OY 1141 TTGACTACTGCTTTTATTTAATACAGTTTTCAGAAACCCCTGAAGTTTAAGTTCA 1200
DB 1141 TTGACTACTGCTTTTATTTAATACAGTTTTCAGAAACCCCTGAAGTTTAAGTTCA 1200
OY 1201 TTATTTCTTATTAACATTTGAGAGAAATGAGATGATGATGAGAGGCTGGGCGAAGA 1260
DB 1201 TTATTTCTTATTAACATTTGAGAGAAATGAGATGATGATGAGAGGCTGGGCGAAGA 1260
OY 1261 CAGGGGCACTAGCTGCTTATTAAGTATTTAGTCCCTCCGCTGTTAGCTTACGCTTTG 1320
DB 1261 CAGGGGCACTAGCTGCTTATTAAGTATTTAGTCCCTCCGCTGTTAGCTTACGCTTTG 1320
OY 1321 ACCCTTCTCTTATATCACAATAATATCAATTAAGCTGAAATTCACATCAATGCTATTT 1380
DB 1321 ACCCTTCTCTTATATCACAATAATATCAATTAAGCTGAAATTCACATCAATGCTATTT 1380

Db 131 ACCCTTCCCTTTGATCCACAAATACATTAATACTGTAATTCACATACATGCTATT 1380
Oy 1381 TAAAGTCATAGATTTAGCTATAAGTCTGACACAGTAATGCTGTAATTTGCT 1440
Db 1381 TAAAGTCATAGATTTAGCTATAAGTCTGACACAGTAATGCTGTAATTTGCT 1440
Oy 1441 ATGTGCCCCACATCGCCCCCACTGGATGGGGTCCAGAGGTTGAGTTCACTATT 1500
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Oy 1501 AACCAATGTCATTAATATCTCTAGAGGTGACAGTGCATATATCTGATG 1560
Db 1501 AACCAATGTCATTAATATCTCTAGAGGTGACAGTGCATATATCTGATG 1560
Oy 1561 TTGACACAGGATTTTATCTGAAGAATACATCTATTAATTAATCTAGAGAAG 1620
Db 1561 TTGACACAGGATTTTATCTGAAGAATACATCTATTAATTAATCTAGAGAAG 1620
Oy 1621 ATTTGACCTGGCTTTAGATTAATACTGTGCAAGAAAATGTATAGCAATATAGAA 1680
Db 1621 ATTTGACCTGGCTTTAGATTAATACTGTGCAAGAAAATGTATAGCAATATAGAA 1680
Oy 1681 ATTAACACACCTTTGTTAAATATAAAAAA 1712
Db 1681 ATTAACACACCTTTGTTAAATATAAAAAA 1712
RESULT 2
AA95787
ID AA95787 standard; cDNA: 1760 BP.
XX
AA95787;
XX
28-FEB-2001 (first entry)
XX
Human immune system molecule cDNA from Incyte clone 1890540.
XX
Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;
XX
antiartherosclerotic; antidiabetic; nephrotropic; cancer;
XX
antigout; dermatological; antihypertensive; hepatotropic; antibody;
XX
immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;
XX
gene therapy; diagnostic; immunological disorder; viral infection; ss;
XX
bacterial infection; fungal infection; parasitic infection; immunogen.
XX
Homo sapiens.
XX
WO200060080-A2.
XX
12-OCT-2000.
XX
PD
XX
04-APR-2000; 2000WO-US09072.
XX
PE
XX
05-APR-1999; 99US-0127852.
XX
PR
XX
05-MAY-1999; 99US-0132647.
XX
PA
XX
(INCY-) INCYTE PHARM INC.
XX
PI
XX
Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DM:
XX
WPI: 2000-665005/64.
XX
P-PSDB: AAB15548.
XX
PT
XX
New human immune system molecules 1-15 and polynucleotides encoding
XX
them useful for diagnosing, treating or preventing e.g. immunological
XX
disorders, infections, cell proliferative disorders, microbial
XX
infections
XX
PS
XX
Claim 4: Page 93; 95pp; English.
XX
This sequence represents the cDNA for a human immune system molecule
XX
(IMOL) isolated as clone 1890540 from the Incyte BtAD707 library.
XX
The human IMOLs (AAB1536-B1550) and their encoding polynucleotides
XX
(AA95775-A95789), and compositions comprising them are useful for the

CC diagnosis, treatment or prevention of immunological disorders,
CC infections and cell proliferative disorders, including cancer. The IMOL
CC may be used to treat or prevent disorders associated with decreased
CC expression or activity of IMOL, such as immunological disorders
CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,
CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
CC Shigella), fungi (e.g. Aspergillus, Blastomycetes), parasites (e.g.
CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and
CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
CC useful as immunogens for the development of antibodies that
CC specifically recognize these peptides. The polynucleotides may be used
CC to detect and quantify gene expression in biopsied tissues in which
CC expression of IMOL may be correlated with the disease, as targets in a
CC microarray, to detect differences in gene sequences among normal,
CC carrier and affected individuals, and for screening libraries of
CC compounds in drug screening techniques. Antibodies which specifically
CC bind to IMOL may be used for the diagnosis of disorders characterized
CC by expression of IMOL, or in assays to monitor patients being treated
CC with IMOL or agonists, antagonists, or inhibitors of IMOL.
XX
SQ Sequence 1760 BP; 505 A; 376 C; 395 G; 484 T; 0 other:
Query Match 99.9%; Score 1710.4; DB 21; Length 1760;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1711; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GGCATGCGCCGAGAGACACCGCTCTGAGCTGCTGCTCTTCACAGGAGACTCTGA 60
Db 48 GGCATGCGCCGAGAGACACCGCTCTGAGCTGCTGCTCTTCACAGGAGACTCTGA 107
Oy 61 GGCCTGTGAGATCATGCTTTGGAGGAGCATCTATTTGAGCACTGCTGCTTTGTT 120
Db 108 GGCCTGTGAGATCATGCTTTGGAGGAGCATCTATTTGAGCACTGCTGCTTTGTT 167
Oy 121 TTTCTCCCTTTTGGCTGTCAAGATTAATACATGAGTCTCCACAAACCGAGACT 180
Db 168 TTTCTCCCTTTTGGCTGTCAAGATTAATACATGAGTCTCCACAAACCGAGACT 227
Oy 181 ACCCCAGACTCAGTAAGTGTGTATGAGACTACACTTTGAGGCTTACCAAGCCC 240
Db 228 ACCCCAGACTCAGTAAGTGTGTATGAGACTACACTTTGAGGCTTACCAAGCCC 287
Oy 241 CCTGGGCGACGGGCGCTCTGCGATTCAGCAACCAATGAGAAACAAAGCAATGG 300
Db 288 CCTGGGCGACGGGCGCTCTGCGATTCAGCAACCAATGAGAAACAAAGCAATGG 347
Oy 301 AGCAGCTGTCATGAAGAGCCAAAGTGAGAGGCGCAAAAGTGACCTGGGCTCG 360
Db 348 AGCAGCTGTCATGAAGAGCCAAAGTGAGAGGCGCAAAAGTGACCTGGGCTCG 407
Oy 361 AGGCGAGCGGGGCGACATGCGCCCAAGAGAGAAAGGCTACCCGGGATTCACACAG 420
Db 408 AGGCGAGCGGGGCGACATGCGCCCAAGAGAGAAAGGCTACCCGGGATTCACACAG 467
Oy 421 ACTTCAGATTGATTCATGAGGCTTCTGTGCAACCCACTTCAGCAATCAGAAAGTGGAT 480
Db 468 ACTTCAGATTGATTCATGAGGCTTCTGTGCAACCCACTTCAGCAATCAGAAAGTGGAT 527
Oy 481 TATCTTCACAGTGTGAGAGCCAAATGGAACCTTTTGATGTCATGAGTGTAGATT 540
Db 528 TATCTTCACAGTGTGAGAGCCAAATGGAACCTTTTGATGTCATGAGTGTAGATT 587
Oy 541 TGGGGCCCCAGTACAGTGTGTATTTCTTCACCTTCAGCATGATACAGTATGAGATG 600
Db 588 TGGGGCCCCAGTACAGTGTGTATTTCTTCACCTTCAGCATGATACAGTATGAGATG 647
Oy 601 TGAGGAAGTATGATGATCTTATGCAATGGCAACAGTCTTACAGATGAGAGCTTA 660
Db 648 TGAGGAAGTATGATGATCTTATGCAATGGCAACAGTCTTACAGATGAGAGCTTA 707
Oy 661 TGAATGAAGGGCAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAACCAAG 720

|||||
 Db 708 TGAATGAAAGGCAATACATACATCCAGCAATACGCTGCTGAGCTAGCCAAAG 767
 Qy 721 GGATGAGGTTGGCTGGCAATGGGCAATGGCGCTCTCCATGGGACCACACCGCTTCTC 780
 Db 768 GGATGAGGTTGGCTGGCAATGGGCAATGGCGCTCTCCATGGGACCACACCGCTTCTC 827
 Qy 781 CACCTTGGCAAGATCTCTGCTTGAAGTAAATATATGACATGAGTAATGCTTCAC 840
 Db 828 CACCTTGGCAAGATCTCTGCTTGAAGTAAATATATGACATGAGTAATGCTTCAC 887
 Qy 841 TTGGGGAAGACTGTAGCTAGCTGATGTTGTTACGATCTGAGGAACATTAAGTTGAG 900
 Db 888 TTGGGGAAGACTGTAGCTAGCTGATGTTGTTACGATCTGAGGAACATTAAGTTGAG 947
 Qy 901 GTTTTACATGCTGTATTCAAAAATATATGTTGCTTGTTCACGCTACAGGTACA 960
 Db 948 GTTTTACATGCTGTATTCAAAAATATATGTTGCTTGTTCACGCTACAGGTACA 1007
 Qy 961 CCATTAATGTTGCAATTCAGGGGCTCAGAGATCAACCAAAATAGCTTCTCAGA 1020
 Db 1008 CCATTAATGTTGCAATTCAGGGGCTCAGAGATCAACCAAAATAGCTTCTCAGA 1067
 Qy 1021 TGACCTGACTAATATATACATGATCTTATCCTCTTCTGGCACTAAAGATAT 1080
 Db 1068 TGACCTGACTAATATATACATGATCTTATCCTCTTCTGGCACTAAAGATAT 1127
 Qy 1081 TCTCTCTGACGAGGTTGGAATATTTTCTATCAGAGATCAATTTGCAAGATTT 1140
 Db 1128 TCTCTCTGACGAGGTTGGAATATTTTCTATCAGAGATCAATTTGCAAGATTT 1187
 Qy 1141 TTGCTCTCTGCTTTTAAATTAATACAGTTCAGAGATCCCTGAGTTTAAGTTCA 1200
 Db 1188 TTGCTCTCTGCTTTTAAATTAATACAGTTCAGAGATCCCTGAGTTTAAGTTCA 1247
 Qy 1201 TTATCTTTTAAACATTTGAGAGATGATGATGATGATGATGATGATGATGATGAT 1260
 Db 1248 TTATCTTTTAAACATTTGAGAGATGATGATGATGATGATGATGATGATGATGAT 1307
 Qy 1261 CAGGGGCACTAGCTGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
 Db 1308 CAGGGGCACTAGCTGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1367
 Qy 1321 ACCCTTCTTGTGATCCAAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
 Db 1368 ACCCTTCTTGTGATCCAAATATATTAATTAATTAATTAATTAATTAATTAATTAAT 1427
 Qy 1381 TAAAGTCATATGATTTAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTTGT 1440
 Db 1428 TAAAGTCATATGATTTAGCTATTAATTAATTAATTAATTAATTAATTAATTTGT 1487
 Qy 1441 ATGTTCCCCCACTGCGCCCACTTGGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1488 ATGTTCCCCCACTGCGCCCACTTGGATGATGATGATGATGATGATGATGATGAT 1547
 Qy 1501 AACAAATGTCATTAATATCTATGAGTACAGTCCCAATGATTAATCAATGTTGATG 1560
 Db 1548 AACAAATGTCATTAATATCTATGAGTACAGTCCCAATGATTAATCAATGTTGATG 1607
 Qy 1561 TTGACCAAGAGGATTTTATATCTGAAAGACATACATTAATTAATTAATTAATTAAT 1620
 Db 1608 TTGACCAAGAGGATTTTATATCTGAAAGACATACATTAATTAATTAATTAATTAAT 1667
 Qy 1621 ATTTTGACCTGGCTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
 Db 1668 ATTTTGACCTGGCTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1727
 Qy 1681 ATTAACACACCTTTGTTAAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1712
 Db 1728 ATTAACACACCTTTGTTAAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1759

RESULT 3

AAC64058
 ID AAC64058 standard; cDNA; 1696 BP.
 XX
 AC AAC64058;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Human zacr3p3 cDNA, SEQ ID NO:1.
 XX
 KW Human zacr3p3; adipocyte complement related protein homologue;
 KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;
 KW cellular metabolism; metabolic disorder; obesity; anorexia;
 KW antimicrobial agent; infection; platelet aggregation inhibition;
 KW adhesion; activation; vascular injury; antibacterial; antiviral; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200063377-A1.
 XX
 PD 26-OCT-2000.
 XX
 PE 19-APR-2000; 2000WO-US10454.
 XX
 PR 20-APR-1999; 99US-0294943.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Piddington CS, Bishop PD;
 XX
 DR WPI: 2000-665243/64.
 DR P-PSDB; AAB29580.
 PT Novel zacr3p3 polypeptides used to treat or prevent bacterial or viral
 PT infections, for wound healing, improving blood flow, and to analyze
 PT energy efficiency in mammals -
 XX
 PS Claim 31: Page 107-109; 123pp; English.
 XX
 CC The invention relates to the human zacr3p3 protein (AAB29580) and to
 CC nucleic acids which encode it (AAC64058; AAC64063). Zacr3p3 is a homologue
 CC of adipocyte complement related protein (ACRP30) and contains a
 CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
 CC C-terminal C1q domain comprising 10 beta-strands. The zacr3p3 gene is
 CC located on chromosome 5p12. The invention also relates to zacr3p3
 CC fragments, fusion proteins containing zacr3p3 polypeptides,
 CC zacr3p3-specific antibodies, expression constructs and host cells
 CC comprising zacr3p3 nucleic acids, and methods of recombinant production of
 CC zacr3p3. Human zacr3p3, and its agonists and antagonists may be used in the
 CC study and modulation of cellular metabolism and energy balance in
 CC mammals, and may therefore be used to treat disorders such as obesity and
 CC anorexia, and conditions associated with these disorders. Due to its C1q
 CC like domain, zacr3p3 and zacr3p3-containing fusion proteins may be useful
 CC as antimicrobial agents, promoting lysis or phagocytosis of infectious
 CC organisms such as bacteria or viruses. Zacr3p3, its fragments, fusion
 CC proteins, antibodies and activity modulators may also be used to inhibit
 CC collagen-induced platelet aggregation, adhesion, or activation, and may
 CC therefore have potential for promoting blood flow within the vasculature
 CC of a mammal e.g., to treat injury to the vasculature or other collagenous
 CC tissue. Human zacr3p3 and its antibodies may additionally be used to study
 CC dimerisation and oligomerisation. The present sequence represents cDNA
 CC encoding human zacr3p3.
 XX
 SQ Sequence 1696 BP; 482 A; 355 C; 386 G; 473 T; 0 other;
 Query Match 99.1%; Score 1696; DB 21; Length 1696;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 CCCGAGGAGACGACGCTCCGAGCTGCTGCTTCCAGGAGACGCTAGCGTCTGT 68
 Db 1 CCCGAGGAGACGACGCTCCGAGCTGCTGCTTCCAGGAGACGCTAGCGTCTGT 60
 Qy 69 TGAGATCATGCTTTGGAGGAGCTCATCTATTGGCAACTGCTGCTTTGTTTCTCTC 128

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Db 1141 TCGCTTTTAATTAAATACAGTTTTCAGAACCCCTGAAGTTTAAGTTCATTATCTT 1200
QY 1209 TATAACATTTGAGAGAAATCGATGCTAGTATGATGACAGGCTGGGCAAGACAGGGCA 1268
Db 1201 TATACATTTTGAGAGATTCGGATGTACTGATATGACAGGGCTGGGCAAGACAGGGCA 1260
QY 1269 CTAGCTCCCTTATTAAGTAAATTAAGTCCCTCCGCTGTTCAAGCTTAAGCTTTGACCCTTTTC 1328
Db 1261 CTAGCTCCCTTATTAAGTAAATTAAGTCCCTCCGCTGTTCAAGCTTAAGCTTTGACCCTTTTC 1320
QY 1329 CTTTTCATCCACAATAATACATTAATAACTCTGTAATTCACATACAAATGCTATTTTAAATGCA 1388
Db 1321 CTTTTCATCCACAATAATACATTAATAACTCTGTAATTCACATACAAATGCTATTTTAAATGCA 1380
QY 1389 ATGATTTTACCTTAATTAAGCTTGACACAGTAATGCTGTTGTAATTTTGTATGTTCC 1448
Db 1381 ATGATTTTACCTTAATTAAGCTTGACACAGTAATGCTGTTGTAATTTTGTATGTTCC 1440
QY 1449 CCACATGCCCCCACTTCGGATGAGGCTGACAGAGCTTGAGGTTCACTATTAACAATG 1508
Db 1441 CCACATGCCCCCACTTCGGATGAGGCTGACAGAGCTTGAGGTTCACTATTAACAATG 1500
QY 1509 TCATTAATATCTCATYAGAGTACAGTCCCAATAGATATTCAAATGTTGCATGTTGACCA 1568
Db 1501 TCATTAATATCTCATYAGAGTACAGTCCCAATAGATATTCAAATGTTGCATGTTGACCA 1560
QY 1569 AGGATTTTATCTATCTGAAGAACAATACATCTTAATAATACCTTAAGCAAAAGATTTTGC 1628
Db 1561 AGGATTTTATCTATCTGAAGAACAATACATCTTAATAATACCTTAAGCAAAAGATTTTGC 1620
QY 1629 CTGGCTTTAGATAAATCTGTGCAAGAAATAATGAAGCAATATATGAAATAAATGCA 1688
Db 1621 CTGGCTTTAGATAAATCTGTGCAAGAAATAATGAAGCAATATATGAAATAAATGCA 1680
QY 1689 ACCTTTGTTAAGATA 1704
Db 1681 ACCTTTGTTAAGATA 1696

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Db 1141 TCGCTTTTAATTAAATACAGTTTTCAGAACCCCTGAAGTTTAAGTTCATTATCTT 1200
QY 1209 TATAACATTTGAGAGAAATCGATGCTAGTATGATGACAGGCTGGGCAAGACAGGGCA 1268
Db 1201 TATACATTTTGAGAGATTCGGATGTACTGATATGACAGGGCTGGGCAAGACAGGGCA 1260
QY 1269 CTAGCTCCCTTATTAAGTAAATTAAGTCCCTCCGCTGTTCAAGCTTAAGCTTTGACCCTTTTC 1328
Db 1261 CTAGCTCCCTTATTAAGTAAATTAAGTCCCTCCGCTGTTCAAGCTTAAGCTTTGACCCTTTTC 1320
QY 1329 CTTTTCATCCACAATAATACATTAATAACTCTGTAATTCACATACAAATGCTATTTTAAATGCA 1388
Db 1321 CTTTTCATCCACAATAATACATTAATAACTCTGTAATTCACATACAAATGCTATTTTAAATGCA 1380
QY 1389 ATGATTTTACCTTAATTAAGCTTGACACAGTAATGCTGTTGTAATTTTGTATGTTCC 1448
Db 1381 ATGATTTTACCTTAATTAAGCTTGACACAGTAATGCTGTTGTAATTTTGTATGTTCC 1440
QY 1449 CCACATGCCCCCACTTCGGATGAGGCTGACAGAGCTTGAGGTTCACTATTAACAATG 1508
Db 1441 CCACATGCCCCCACTTCGGATGAGGCTGACAGAGCTTGAGGTTCACTATTAACAATG 1500
QY 1509 TCATTAATATCTCATYAGAGTACAGTCCCAATAGATATTCAAATGTTGCATGTTGACCA 1568
Db 1501 TCATTAATATCTCATYAGAGTACAGTCCCAATAGATATTCAAATGTTGCATGTTGACCA 1560
QY 1569 AGGATTTTATCTATCTGAAGAACAATACATCTTAATAATACCTTAAGCAAAAGATTTTGC 1628
Db 1561 AGGATTTTATCTATCTGAAGAACAATACATCTTAATAATACCTTAAGCAAAAGATTTTGC 1620
QY 1629 CTGGCTTTAGATAAATCTGTGCAAGAAATAATGAAGCAATATATGAAATAAATGCA 1688
Db 1621 CTGGCTTTAGATAAATCTGTGCAAGAAATAATGAAGCAATATATGAAATAAATGCA 1680
QY 1689 ACCTTTGTTAAGATA 1704
Db 1681 ACCTTTGTTAAGATA 1696

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RESULT 4
AAFP3874
ID AAFP3874 standard; cDNA: 1709 BP.
XX
AC AAFP3874;
XX
DF 23-MAY-2001 (first entry)
XX
DE Human cDNA encoding a membrane or secretory protein clone PSEC0232.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes; ss.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PE 07-JUL-2000; 2000EP-0114090.
XX
PR 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR WPI: 2001-093989/11.
XX
P-PSDB: AAB8447.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
gene therapy or as candidate target molecules in drug development -

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XX Claim 1; SEQ ID 261; 609pp + CD ROM; English.
PS

This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies (agonists and antagonists) may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.

Sequence 1709 BP; 480 A; 363 C; 390 G; 476 T; 0 other;

Query Match	99.0%	Score	1695.4	DB	22	Length	1709
Best Local Similarity	99.98%	Pred.	No. 0				
Matches 1696: Conservative	0	Mismatches	1	Indels	0	Gaps	0

QY	1	GGATATGCCCCGAGAGAACCAAGCTCCTGGAGCTGTGCTGTCTTCTTCAGGAGAGACTCTGA	60
Db	13	GGCATTCGCCCGAGAGAACCAAGCTCCTCCGGAGCTGTGCTGTCTTCTTCAGGAGAACCTCTGA	72
QY	61	GGCATCTGTGGAAATCATATGCTTTTGGAGGCGAGCTCATCTATATGGCAACTGGTGGCTTTGTT	120
Db	73	GGCTCTGTGGAAATCATATGCTTTTGGAGGCGAGCTCATCTATATGGCAACTGCTGGCTTTGTT	132
QY	121	TTTTCTCCCTTTTGGCTGTGTCAAGATGAATACATGAGTCTCCACAAACCGGAGAGCT	180
Db	133	TTTTCTCCCTTTTGGCTGTGTCAAGATGAATACATGAGTCTCCACAAACCGGAGAGACT	192
QY	181	ACCCCCAGACTGCGAGTAAGTGTGTCTATGGAGACTACAGCTTTTCGAGGCTACCAAGGCC	240
Db	193	ACCCCCAGACTGCGAGTAAGTGTGTCTATGGAGACTACAGCTTTTCGAGGCTACCAAGGCC	252
QY	241	CCCTGGGACCAACGGGCGCTCCTGGCATTTCCAGGAAACATGAAACATATGGCAACAATGS	300
Db	253	CCCTGGGACCAACGGGCGCTCCTGGCATTTCCAGGAAACATGAAACATATGGCAACAATGS	312
QY	301	AGCCATGTGTCATTAAGAGAGCCAAAGGTGAAGAGGGCGACAAAGGTGACCTTGGGGCCTCG	360
Db	313	AGCCATGTGTCATTAAGAGAGCCAAAGGTGAAGAGGGCGACAAAGGTGACCTTGGGGCCTCG	372
QY	361	AGGGGAGCGGGGGGCGAGCATGGGCCCCAAAGAGAGAGAGGGCTACCCGGGGATTCACACCA	420
Db	373	AGGGGAGCGGGGGGCGAGCATGGGCCCCAAAGAGAGAGAGGGCTACCCGGGGATTCACACCA	432
QY	421	ACCTTCAGATTTCATTCATGGCTTCTCGGGAACCCACTTCAGCAATTCAGAAACAGTGGGAT	480
Db	433	ACCTTCAGATTTCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATTCAGAAACAGTGGGAT	492
QY	481	TATCTTCAGCAGTGTGAGAGCAACAATTTGGAACCTTCTTGATGATCATGACTGGTAGATT	540
Db	493	TATCTTCAGCAGTGTGAGAGCAACAATTTGGAACCTTCTTGATGATCATGACTGGTAGATT	552
QY	541	TGGGGCCCCAGTATACAGGTGTATTTTCTTCACCTTCAGCATATGAGCATGAGCATGT	600
Db	553	TGGGGCCCCAGTATACAGGTGTATTTTCTTCACCTTCAGCATATGAGCATGAGCATGT	612

QY	601	7GAGGAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTGACGATGTACAGCTA	660
Db	613	7GAGGAGAGTATGTGTACCTTATGCACAATGGCAACACAGTCTTGACGATGTACAGCTA	672
QY	661	7GAAATGAAAGGGCCAATTCAGATACATCCAGCAATCAATGCGTGTCTCAAGCTACCAAGG	720
Db	673	7GAAATGAAAGGGCCAATTCAGATACATCCAGCAATCAATGCGTGTCTCAAGCTACCAAGG	732
QY	721	GGATGAGGTTTGGCTGTGCGAATGGGCAATGGCGCTCCCATGGGGACCAACGCTTCTC	780
Db	733	GGATGAGGTTTGGCTGTGCGAATGGGCAATGGCGCTCCCATGGGGACCAACGCTTCTC	792
QY	781	CACCTTGGAGGATTCCTCTCTTTGAACCTAGTAAATATATAGCTAGAAATAGCTCCAC	840
Db	793	CACCTTGGAGGATTCCTCTCTTTGAACCTAGTAAATATATAGCTAGAAATAGCTCCAC	852
QY	841	TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACATCGAGGAACATTTAAAGTTGAGG	900
Db	853	TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACATCGAGGAACATTTAAAGTTGAGG	912
QY	901	GTTTTCATTTGCTGTATTTCAAAAAATTTATTTGGTTCGAATGTGTTCAAGCTACAGGTACA	960
Db	913	GTTTTCATTTGCTGTATTTCAAAAAATTTATTTGGTTCGAATGTGTTCAAGCTACAGGTACA	972
QY	961	CCAAATPATTTTGACCAATTCAGGGGCTCAGAAAGATCAACACCAAAATATGTTCTTCAGA	1020
Db	973	CCAAATPATTTTGACCAATTCAGGGGCTCAGAAAGATCAACACCAAAATATGTTCTTCAGA	1032
QY	1021	TGACCTTGACTAATATATCTAGCATCTTATATCACTCTTTCCTTGGCACTTAAAAAGATAT	1080
Db	1033	TGACCTTGACTAATATATCTAGCATCTTATATCACTCTTTCCTTGGCACTTAAAAAGATAT	1092
QY	1081	TCTCCCTTCAGCAGGTGGAATATTTTTTCTATCACAAGAGCTATTTGCAAGATTT	1140
Db	1093	TCTCCCTTCAGCAGGTGGAATATTTTTTCTATCACAAGAGCTATTTGCAAGATTT	1152
QY	1141	TTGACTACTCTCTTTTAAATTTAATACAGTTTTCAGAAACCCCTCAAGTTTAAAGTTCA	1200
Db	1153	TTGACTACTCTCTCTTTTAAATTTAATACAGTTTTCAGAAACCCCTCAAGTTTAAAGTTCA	1212
QY	1201	TTATTTCTTTATAACATTGAGAGAAATCGATGTAGTATATGACAGGCTGGGGCAAGAA	1260
Db	1213	TTATTTCTTTATAACATTGAGAGAAATCGATGTAGTATATGACAGGCTGGGGCAAGAA	1272
QY	1261	CAGGGCAGCTAGCTGCTTATTGCTAATTTAGTGGCCTCGGTTCAGCTTAAAGCTTTG	1320
Db	1273	CAGGGCAGCTAGCTGCTTATTGCTAATTTAGTGGCCTCGGTTCAGCTTAAAGCTTTG	1332
QY	1321	ACCTTTCTCTTTGATTCACAAAAATACATTTAAAACTGTGATTTACATACATGCTATTTT	1380
Db	1333	ACCTTTCTCTTTGATTCACAAAAATACATTTAAAACTGTGATTTACATACATGCTATTTT	1392
QY	1381	TAAAGTCATATAGTTTATAGCTATAAAGTGTTCACAGAGTAATGTGGTATTAATTTGTGT	1440
Db	1393	TAAAGTCATATAGTTTATAGCTATAAAGTGTTCACAGAGTAATGTGGTATTAATTTGTGT	1452
QY	1441	ATGTTTCCCCACATCGCCCCCAACTTTCGGAATGTGGGGTCAAGAGGTTGAGGTTCACTATT	1500
Db	1453	ATGTTTCCCCACATCGCCCCCAACTTTCGGAATGTGGGGTCAAGAGGTTGAGGTTCACTATT	1512
QY	1501	AACAAATGTCAATTAATATCTCATATAGAGTACAGTGGCCAATAGATATTTCAATGTGTGATG	1560
Db	1513	AACAAATGTCAATTAATATCTCATATAGAGTACAGTGGCCAATAGATATTTCAATGTGTGATG	1572
QY	1561	TTGACAGAGGAGTTTATATCTGAGAAGACATACACTATTAATTAATACCTTGAGAGAAAG	1620
Db	1573	TTGACAGAGGAGTTTATATCTGAGAAGACATACACTATTAATTAATACCTTGAGAGAAAG	1632
QY	1621	ATTTTGACCTGCTTTAGTATAAACTGTGGCAAGAAAATGTATATGACAAATATATGAA	1680
Db	1633	ATTTTGACCTGCTTTAGTATAAACTGTGGCAAGAAAATGTATATGACAAATATATGAA	1692

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Oy 1681 ATAAACACACCTTTGTT 1697
      |||||
Db 1693 ATAAACACACCTTTGTT 1709

RESULT 5
AAI99523
ID AAI99523 standard; cDNA; 1620 BP.
XX
AC AAI99523;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 21.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antinflammatory; antiulcer;
KW vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; Cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ss.
XX
OS Homo sapiens.
XX
PN WO20015173-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001: 2001WO-US01356.
XX
PR 31-JAN-2000: 2000US-0179065.
PR 04-FEB-2000: 2000US-0180628.
PR 24-FEB-2000: 2000US-0184664.
PR 02-MAR-2000: 2000US-0186350.
PR 16-MAR-2000: 2000US-0189874.
PR 17-MAR-2000: 2000US-0190076.
PR 18-APR-2000: 2000US-0198123.
PR 19-MAY-2000: 2000US-0205515.
PR 07-JUN-2000: 2000US-0209467.
PR 28-JUN-2000: 2000US-0214886.
PR 30-JUN-2000: 2000US-0215135.
PR 07-JUL-2000: 2000US-0216647.
PR 07-JUL-2000: 2000US-0216880.
PR 11-JUL-2000: 2000US-0217487.
PR 11-JUL-2000: 2000US-0217496.
PR 14-JUL-2000: 2000US-0218290.
PR 26-JUL-2000: 2000US-0220963.
PR 26-JUL-2000: 2000US-0220964.
PR 14-AUG-2000: 2000US-0224518.
PR 14-AUG-2000: 2000US-0224519.
PR 14-AUG-2000: 2000US-0225213.
PR 14-AUG-2000: 2000US-0225214.
PR 14-AUG-2000: 2000US-0225266.
PR 14-AUG-2000: 2000US-0225267.
PR 14-AUG-2000: 2000US-0225268.
PR 14-AUG-2000: 2000US-0225270.
PR 14-AUG-2000: 2000US-0225447.
PR 14-AUG-2000: 2000US-0225757.
PR 14-AUG-2000: 2000US-0225758.
PR 14-AUG-2000: 2000US-0225759.
PR 18-AUG-2000: 2000US-0226279.
PR 22-AUG-2000: 2000US-0226681.
PR 22-AUG-2000: 2000US-0226686.
PR 22-AUG-2000: 2000US-0227182.
PR 23-AUG-2000: 2000US-0227009.
PR 30-AUG-2000: 2000US-0228924.
PR 01-SEP-2000: 2000US-0229287.
PR 01-SEP-2000: 2000US-0229343.
PR 01-SEP-2000: 2000US-0229344.
PR 01-SEP-2000: 2000US-0229345.
PR 05-SEP-2000: 2000US-0229509.
PR 05-SEP-2000: 2000US-0229513.
PR 06-SEP-2000: 2000US-0230437.
PR 06-SEP-2000: 2000US-0230438.
PR 08-SEP-2000: 2000US-0231242.
PR 08-SEP-2000: 2000US-0231243.
PR 08-SEP-2000: 2000US-0231244.
PR 08-SEP-2000: 2000US-0231413.
PR 08-SEP-2000: 2000US-0231414.
PR 08-SEP-2000: 2000US-0232080.
PR 08-SEP-2000: 2000US-0232081.
PR 12-SEP-2000: 2000US-0231968.
PR 14-SEP-2000: 2000US-0232397.
PR 14-SEP-2000: 2000US-0232398.
PR 14-SEP-2000: 2000US-0232399.
PR 14-SEP-2000: 2000US-0232400.
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PR 14-SEP-2000: 2000US-0233063.
PR 14-SEP-2000: 2000US-0233064.
PR 14-SEP-2000: 2000US-0233065.
PR 21-SEP-2000: 2000US-0234223.
PR 21-SEP-2000: 2000US-0234274.
PR 25-SEP-2000: 2000US-0234997.
PR 25-SEP-2000: 2000US-0234998.
PR 26-SEP-2000: 2000US-0235484.
PR 27-SEP-2000: 2000US-0235834.
PR 27-SEP-2000: 2000US-0235836.
PR 29-SEP-2000: 2000US-0236327.
PR 29-SEP-2000: 2000US-0236367.
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PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
PR 02-OCT-2000: 2000US-0237040.
PR 13-OCT-2000: 2000US-0239935.
PR 13-OCT-2000: 2000US-0239937.
PR 20-OCT-2000: 2000US-0240960.
PR 20-OCT-2000: 2000US-0241221.
PR 20-OCT-2000: 2000US-0241785.
PR 20-OCT-2000: 2000US-0241786.
PR 20-OCT-2000: 2000US-0241787.
PR 20-OCT-2000: 2000US-0241808.
PR 20-OCT-2000: 2000US-0241809.
PR 20-OCT-2000: 2000US-0241826.
PR 01-NOV-2000: 2000US-0244617.
PR 08-NOV-2000: 2000US-0244674.
PR 08-NOV-2000: 2000US-0246475.
PR 08-NOV-2000: 2000US-0246476.
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PR 08-NOV-2000: 2000US-0246478.
PR 08-NOV-2000: 2000US-0246523.
PR 08-NOV-2000: 2000US-0246524.
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PR 08-NOV-2000: 2000US-0246527.
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PR 08-NOV-2000: 2000US-0246609.
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PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
PR 17-NOV-2000: 2000US-0249209.
PR 17-NOV-2000: 2000US-0249210.
PR 17-NOV-2000: 2000US-0249211.
PR 17-NOV-2000: 2000US-0249212.
PR 17-NOV-2000: 2000US-0249213.
PR 17-NOV-2000: 2000US-0249214.
PR 17-NOV-2000: 2000US-0249215.
PR 17-NOV-2000: 2000US-0249216.
PR 17-NOV-2000: 2000US-0249217.
PR 17-NOV-2000: 2000US-0249218.
PR 17-NOV-2000: 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 06-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251899.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Barash SC, Ruben SM;

PI WPI: 2001-451924/48.

XX P-PSDB; AAM99925.

PT New nucleic acids and polypeptides, useful for treating, preventing or
 DR ameliorating human disorders and diseases -
 XX
 PS Claim 1; SEQ ID NO 21; 465bp + Sequence Listing; English.

CC The invention relates to novel human polynucleotides (AA195513-AA19538)
 CC and the encoded proteins (AAM9915-AAM9934) which are useful for
 CC preventing, treating or ameliorating medical conditions e.g. by protein
 CC or gene therapy. The genes are isolated from a range of human tissues
 CC disclosed in the specification. The nucleic acids, proteins, antibodies
 CC and (antagonists are useful in the diagnosis, treatment and prevention
 CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
 CC myocardial ischaemia; (d) wound healing; (e) neurological diseases
 CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as
 CC viral, bacterial, fungal and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ffp.wipo.int/pub/published_pct_sequences.

XX Sequence 1620 BP; 485 A; 332 C; 360 G; 440 T; 3 other;

Query Match 90.5%; Score 1549.6; DB 22; Length 1620;

Best Local Similarity 99.7%; Pred. No. 0; Matches 1549; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 159 AGTCTCCAAACCGGAGAGTACCCCGACAGTCACTAGTGTGTCATGAGAGACTACA 218
 DB 22 AGTCTCCAAACCGGAGAGTACCCCGACAGTCACTAGTGTGTCATGAGAGACTACA 81
 OY 219 GCTTTCAGGTACCAAGGCGCCCGTGGGCGACAGGGGCGCCCTGGGATTCAGAGAAC 278
 DB 82 GCTTTCAGGTACCAAGGCGCCCGTGGGCGACAGGGGCGCCCTGGGATTCAGAGAAC 141
 OY 279 ATGGAACAATGCGACATGAGCCACTGTCTATGAAGAGCCAAAGGTGAGAGGGCG 338
 DB 142 ATGGAACAATGCGACATGAGCCACTGTCTATGAAGAGCCAAAGGTGAGAGGGCG 201
 OY 339 ACAAGGTGAGTGGGCGCTGAGAGGAGCGGGGCGAGCATGCGCCCAAGAGAGAGAGG 398
 DB 202 ACAAGGTGAGTGGGCGCTGAGAGGAGCGGGGCGAGCATGCGCCCAAGAGAGAGAGG 261

OY 399 GCTACCCGGGAGTTCCACGAACTTCAGATTGATTCCTCTGCGAACCCACT 458
 DB 262 GCTACCCGGGAGTTCCACGAACTTCAGATTGATTCCTCTGCGAACCCACT 321
 OY 459 TCAGCAATCAGAACAGTGGGATTAATCTTCACAGAGTGTGAGACCACATTTGGAACTTCT 518
 DB 322 TCAGCAATCAGAACAGTGGGATTAATCTTCACAGAGTGTGAGACCACATTTGGAACTTCT 381
 OY 519 TTGATGTCAATGACTGTGAGATTTGGGGCCCGAGTATGAGTGTATTTCTTCACCTTCA 578
 DB 382 TTGATGTCAATGACTGTGAGATTTGGGGCCCGAGTATGAGTGTATTTCTTCACCTTCA 441
 OY 579 GCATGATGAAGCATGAGAGTGTGAGAGAGTGTATGTTACTTATTCACATGAGCAACA 638
 DB 442 GCATGATGAAGCATGAGAGTGTGAGAGAGTGTATGTTACTTATTCACATGAGCAACA 501
 OY 639 CAGTCTTCACATGATGAGCTATGAATGAAGGGCAATCAGATACATCCAGCAATCATG 698
 DB 502 CAGTCTTCACATGATGAGCTATGAATGAAGGGCAATCAGATACATCCAGCAATCATG 561
 OY 699 CTGTGCTGAAGTACGCCAAAGGGGATGAGTTGGCTGCGCAATGGGCGGCTCTCC 758
 DB 562 CTGTGCTGAAGTACGCCAAAGGGGATGAGTTGGCTGCGCAATGGGCGGCTCTCC 621
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 DB 622 ATGGGAGACCAACAGCGCTTCCACCTTTGCGAGATTCCTCTTGAACCTAAGTAAA 681
 OY 819 TATATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGATTTGTACGAT 878
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 OY 939 TGTGTTACAGCTCAGGTACCAATATATGTTGAGCAATTCAGGGGCTCGAAGAAATCA 998
 DB 802 TGTGTTACAGCTCAGGTACCAATATATGTTGAGCAATTCAGGGGCTCGAAGAAATCA 861
 OY 999 ACCAACAATAAGTCTTCTCAGATGACCTGACATATATATCTCAGATCTTATACCTTT 1058
 DB 862 ACCAACAATAAGTCTTCTCAGATGACCTGACATATATATCTCAGATCTTATACCTTT 921
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 DB 922 TCCCTGGCAGCTTAAGATTAATTCCTCTCAGCAGAGTGGAAATATTTTCTCTATCA 981
 OY 1119 CAGAGTCAATTTGGAAGAAATTTGAGTCTGCTTTTAAATTAATTAATCCAGTTTTCAG 1178
 DB 982 CAGAGTCAATTTGGAAGAAATTTGAGTCTGCTTTTAAATTAATTAATCCAGTTTTCAG 1041
 OY 1179 AACCCCTGAAGTTTAAAGTCAATTAATTTAAATTTGAGAGATCGAGTATGTA 1238
 DB 1042 AACCCCTGAAGTTTAAAGTCAATTAATTTAAATTTGAGAGATCGAGTATGTA 1101
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 DB 1282 TAATGTGTTATTTTGTATATCTCCCGACATGCGCCCAATCTGGATGGGGGT 1341
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 OY 1115 ATCAGAGAATCATTTGCAAGAAATTTTGACTACTCTCTTTTAATTAATACAGTTT 1174
 DB 1198 ATCAGAGAATCATTTGCAAGAAATTTTGACTACTCTCTTTTAATTAATACAGTTT 1257
 OY 1175 CAGGAACCCCTGAGATTTTAAGTTCATTTCTTTATACATTGAGAAATCGGATGTA 1234
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 DB 1378 GCCCTCCGTGTTACAGCTTACGCTTTGACCTTTCTTTGATCCAAATATTAATAA 1437
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 OY 1655 AAAAATGTAATGAGCAATATATGAAATTAACACACCTTTGTTAAAGATTAATAA 1709
 DB 1738 AAAAATGTAATGAGCAATATATGAAATTAACACACCTTTGTTAAAGATTAATAA 1792
 RESULT 7
 AAD12584
 ID AAD12584 standard; cDNA; 1927 BP.
 AC AAD12584;
 XX 25-SEP-2001 (first entry)
 DE Human protein having hydrophobic domain encoding cDNA clone HP10781.
 KW Human: hydrophobic domain; gene therapy; nutritional supplement;
 KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; antifertility; antiinflammatory; ss.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 89..760
 FT /tag= a
 FT /product= "Human protein having hydrophobic domain"
 FT /note= "cDS is specifically is claimed in claim 3"
 FT sig_peptide 89..157
 FT /tag= b

FT mat_peptide 158..757
 FT /tag= c
 FT /product= "Mature human protein with hydrophobic domain"
 XX
 XX W0200149728-A2.
 XX
 XX 12-JUL-2001.
 XX
 XX 28-DEC-2000; 2000MO-JP09359.
 XX
 XX 06-JAN-2000; 2000JP-0000585.
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 XX 06-JAN-2000; 2000JP-0000588.
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 XX 11-JAN-2000; 2000JP-0002299.
 XX
 XX 03-FEB-2000; 2000JP-0026862.
 XX
 XX 03-MAR-2000; 2000JP-0058367.
 XX
 XX (PROT-) PROTEGENE INC.
 XX (SAGA) SAGAMI CHEM RES CENT.
 PA
 PA Kato S, Kimura T;
 PI
 XX WPI: 2001-418355/44.
 DR
 DR P-PSDB: AAE06589.
 XX
 XX Human proteins with hydrophobic domains and the nucleic acids encoding
 PT them, useful for preventing diagnosing and treating e.g. cancer.
 PT Alzheimer's and inflammation -
 PT
 XX Claim 4; Page 352-354; 563bp; English.
 PS
 XX The present sequence is human protein with hydrophobic domain encoding
 CC cDNA clone HP10781. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotides and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional
 CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate activin and inhibin activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.
 CC
 XX Sequence 1927 BP; 550 A; 416 C; 452 G; 509 T; 0 other;
 XX
 XX
 XX Query Match 89.2%; Score 1527; DB 22; Length 1927;
 XX Best Local Similarity 99.9%; Pred. No. 0;
 XX Matches 1538; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 OY 159 AGTCTCCACAAACCGGAGGACTACCCCAAGATGAGTGTGATGAGAGACTACA 218
 DB 390 AGTCTCCACAAACCGGAGGACTACCCCAAGATGAGTGTGATGAGAGACTACA 449
 OY 219 GCTTTCGAGGCTACCAAGGCCCCCTGGGCAACGCGGCTCTGAGCAATTCAGGAAC 278
 DB 450 GCTTTCGAGGCTACCAAGGCCCCCTGGGCAACGCGGCTCTGAGCAATTCAGGAAC 509
 OY 279 ATGGAACAATGGAACAATGAGGCACTGTCATGAAGAGCCAAAGTGAGAGGCG 338
 DB 510 ATGGAACAATGGAACAATGAGGCACTGTCATGAAGAGCCAAAGTGAGAGGCG 569
 OY 339 ACAAGAGTACCTGGGCTGAGAGGAGCGGGGCGAGCATGCCCCCAAGAGAGAAAG 398
 DB 570 ACAAGAGTACCTGGGCTGAGAGGAGCGGGGCGAGCATGCCCCCAAGAGAGAAAG 629

QY 399 GCTACCCGGGATTCACACGAACTTCAGATTCATGAGCTCTCTGGCAACCCACT 458
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 Db 630 GCTACCCGGGATTCACACGAACTTCAGATTCATGAGCTCTCTGGCAACCCACT 689
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 QY 519 TTGATGTCACTGATGATGTTGGGGCCCCCATATCAGTGTGATTTCTTCCACTTCA 578
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 Db 749 TTGATGTCACTGATGATGTTGGGGCCCCCATATCAGTGTGATTTCTTCCACTTCA 808
 QY 579 GCATGATGAAGCATGAGATGTTGAGGAAGTGTATGCTCTTTCACATGAGCAATGGCACA 638
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 Db 809 GCATGATGAAGCATGAGATGTTGAGGAAGTGTATGCTCTTTCACATGAGCAATGGCACA 868
 QY 639 GAGTCTTCAGCATGTACAGTATGAAATGAAAGGCAAAATCAGATACATCCAGCAATCATG 698
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 Db 869 CAGTCTTCAGCATGTACAGTATGAAATGAAAGGCAAAATCAGATACATCCAGCAATCATG 928
 QY 699 CTGTGCTGAAGCTACGCCAAAGGGGATGAGTGGCTGGCAATGGGCAATGGGCTCTCC 758
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 Db 929 CTGTGCTGAAGCTACGCCAAAGGGGATGAGTGGCTGGCAATGGGCAATGGGCTCTCC 988
 QY 759 ATGGGAGCCACCAAGCTTCTCCACCTTTGACAGATTCCTGCTCTTGAAGTAAGTAA 818
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 Db 989 ATGGGAGCCACCAAGCTTCTCCACCTTTGACAGATTCCTGCTCTTGAAGTAAGTAA 1048
 QY 819 TATATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGTATTTGTTACGAT 878
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 Db 1049 TATATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGTATTTGTTACGAT 1108
 QY 879 CTAGAGAACATTAAGTTGAGGGTTTACATGCTGTATTCAAAATAATTTATGTTCCAA 938
 |||||||
 Db 1109 CTAGAGAACATTAAGTTGAGGGTTTACATGCTGTATTCAAAATAATTTATGTTCCAA 1168
 QY 939 TGTGTTGTCAGCTACAGGTACACCAATATGTTGACAAATTCAGGGGCTCAGAAATCA 998
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 Db 1169 TGTGTTGTCAGCTACAGGTACACCAATATGTTGACAAATTCAGGGGCTCAGAAATCA 1228
 QY 999 ACCACAAATATGTTCTCTCAGATGACCTTGACTAATATCTCAGCATCTTTATCAGCTT 1058
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 Db 1229 ACCACAAATATGTTCTCTCAGATGACCTTGACTAATATCTCAGCATCTTTATCAGCTT 1288
 QY 1059 TCCTTGGCAGCTAAAGATATCTCTCTGAGCAGAGTTGGAATATTTTCTCTATCA 1118
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 Db 1289 TCCTTGGCAGCTAAAGATATCTCTCTGAGCAGAGTTGGAATATTTTCTCTATCA 1348
 QY 1119 CAGAAGTCATTTGCAAGAAATTTGACTACTCTCTTTTAAATTAATCCAGTTTTCAGG 1178
 |||||||
 Db 1349 CAGAAGTCATTTGCAAGAAATTTGACTACTCTCTTTTAAATTAATCCAGTTTTCAGG 1408
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 |||||||
 Db 1409 AACCCCTGAAGTTTAAATTCATTTATTTATTAACATTTGAGAAATCGGATGTAGTGA 1468
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 |||||||
 Db 1469 TATGACAGGGCTGGGGCAAAACAGGGGCACTAGCTGCTTATTAAGTATTTAGTCCC 1528
 QY 1299 TCCGTGTTGAGCTTAGCTTGAACCTTTCCTTTGATCCCAAAATACATTAAGTCT 1358
 |||||||
 Db 1529 TCCGTGTTGAGCTTAGCTTGAACCTTTCCTTTGATCCCAAAATACATTAAGTCT 1588
 QY 1359 GAATTCACATACATGCTATTTTAAAGTCATATAGATTTTAAAGTCTTGGACAG 1418
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 Db 1589 GAATTCACATACATGCTATTTTAAAGTCATATAGATTTTAAAGTCTTGGACAG 1648
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QY 1479 CAGGAGCTTGAGGTTCACTATTAACAAATGCTCAATAATATCTCATAGAGCTACAGTCCA 1538
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 Db 1769 ATGATATTTCAATGTTGCACTGTTGACACAGAGGATTTTATCTGTGAAGAACTATACCTA 1828
 QY 1599 TTATATAATACCTTAGAGAAAGATTTTGAACCTGCTTTAGATTAACACTGTGCAAGAAA 1658
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 Db 1829 TTATATAATACCTTAGAGAAAGATTTTGAACCTGCTTTAGATTAACACTGTGCAAGAAA 1888
 QY 1659 ATGTAATGAGCAATATATGGAATTAACACACCTTTGTT 1697
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 Db 1889 ATGTAATGAGCAATATATGGAATTAACACACCTTTGTT 1927

RESULT 8
 ABK35221
 ID ABK35221 standard; cDNA: 1608 BP.
 XX
 AC ABK35221:
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human cDNA encoding secreted protein #359.
 XX
 KW Human; secreted protein; gene; ss: nutritional supplement; haemophilia;
 KW Viral Infection; Bacterial Infection; fungal infection; diabetes; asthma;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour;
 KW autoimmune thyroiditis; allergic reaction; neurodegenerative disease;
 KW Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;
 KW coagulation disorder; inflammatory disorder; Crohn's disease; incision;
 KW tissue regeneration; wound healing; burn; haematopoiesis;
 KW myeloid cell deficiency; lymphoid cell deficiency.
 XX
 OS Homo sapiens.
 XX
 PN MO200177288-A2.
 PD 18-OCT-2001.
 XX
 PF 29-MAR-2001: 2001WO-US10224.
 XX
 PR 06-APR-2000: 2000US-195582P.
 XX
 PA (GEMT) GENETICS INST INC.
 XX
 PI Wong GC, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
 XX Gulukota K, Graham JR;
 XX
 DR WPI: 2002-179321/23.
 XX
 PS
 XX
 PT Five hundred and ninety two polynucleotides derived from a variety of
 PT human tissue sources which encode secreted proteins, useful for
 PT treating immune deficiencies and disorders such as autoimmune disorders
 PT
 Claim 1: Page 261-262; 372pp; English.
 CC The invention relates to 592 polynucleotides which have been derived from
 CC a variety of human tissue sources and which encode novel secreted
 CC proteins. The polynucleotides can be used as probes for the
 CC identification and isolation of full length cDNA and genomic DNA. The
 CC polynucleotides and proteins can also be used as nutritional supplements.
 CC The proteins are useful in the treatment of various immune deficiencies
 CC and disorders such as viral infections, bacterial infections, fungal
 CC infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
 CC and conditions (e.g. asthma). They are also useful for treating
 CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
 CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
 CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also

CC useful for tissue regeneration, for wound healing and in the treatment of
 CC burns, incisions and ulcers. The proteins are also useful for regulating
 CC haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
 CC Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
 XX

Sequence 1608 BP: 487 A; 305 C; 339 G; 477 T; 0 other;

Query Match 79.68; Score 1363.2; DB 24; Length 1608;
 Best Local Similarity 99.88; Pred. No. 0;
 Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 61 GGGCTACCCGGGGATCCACAGAACTTCAGATTGATTCATGCTCTCTGSCACCCA 120
QY 457 CTTGAGCAATGAGAAAGTGGGATTAATCTTCAGAGTGTGAGACCAACATGGAACCTT 516
    |||||||
Db 121 CTTGAGCAATGAGAAAGTGGGATTAATCTTCAGAGTGTGAGACCAACATGGAACCTT 180
QY 517 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
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Db 181 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 577 CAGCATGATGAGAGATGAGATGATGAGAGATGATGATGATGATGATGATGATGATGAT 636
    |||||||
Db 241 CAGCATGATGAGAGATGAGATGATGAGAGATGATGATGATGATGATGATGATGATGAT 300
QY 637 CACAGTCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
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Db 301 CACAGTCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 697 TGTGTGCTGAGAGTACGCAAGGGGATGAGTGTGCTGCGAATGGGCAATGGCGCTCT 756
    |||||||
Db 361 TGTGTGCTGAGAGTACGCAAGGGGATGAGTGTGCTGCGAATGGGCAATGGCGCTCT 420
QY 757 CCATGGGAGCACCAACGCTTCTCCACCTTTCAGAGATTCCTGCTTTTGAACATAAGTA 816
    |||||||
Db 421 CCATGGGAGCACCAACGCTTCTCCACCTTTCAGAGATTCCTGCTTTTGAACATAAGTA 480
QY 817 AATATATGATGAGAAATGCTCCACTTGGGGAGACATGATGCTGAGCTGATTTGTAGC 876
    |||||||
Db 481 AATATATGATGAGAAATGCTCCACTTGGGGAGACATGATGCTGAGCTGATTTGTAGC 540
QY 877 ATCTGAGGAGACATTAAGATTGAGGTTTACATGCTGATATTCAAAATAATTTGTTGC 936
    |||||||
Db 541 ATCTGAGGAGACATTAAGATTGAGGTTTACATGCTGATATTCAAAATAATTTGTTGC 600
QY 937 AATGTTGTTACGCTACAGGTACCAACATTAATGTTGACAAATTCAGGGGCTCAGAGAAAT 996
    |||||||
Db 601 AATGTTGTTACGCTACAGGTACCAACATTAATGTTGACAAATTCAGGGGCTCAGAGAAAT 660
QY 997 CAACCAACAATATGCTCTCAGATGACCTGACTAATATCTCAGACATCTTATCATCTC 1056
    |||||||
Db 661 CAACCAACAATATGCTCTCAGATGACCTGACTAATATCTCAGACATCTTATCATCTC 720
QY 1057 TTTCTTGGACCTTAAGATTAATTCCTCTGACGAGTGTGGAATATTTTCTAT 1116
    |||||||
Db 721 TTTCTTGGACCTTAAGATTAATTCCTCTGACGAGTGTGGAATATTTTCTAT 780
QY 1117 CACGAGATGATTTGCAAGAATTTTGCATGCTGCTTTAATTAATACAGCTTTTCA 1176
    |||||||
Db 781 CACGAGATGATTTGCAAGAATTTTGCATGCTGCTTTAATTAATACAGCTTTTCA 840
QY 1177 GGAACCCCTGAGTTTAAAGTCAATTAATTTTATACATTTGAGAAATGAGTGTAGT 1236
    |||||||
Db 841 GGAACCCCTGAGTTTAAAGTCAATTAATTTTATTAACATTTGAGAAATGAGTGTAGT 900
QY 1237 GATATGACAGGGCTGGGCAAGAAGAGGGGCACTAGCTTGTATTAATTAATTTAGTGC 1296
    |||||||

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Db 901 GATATGACAGGGCTGGGGCAAGAACAGGGGACATGCTGCTTATTAATTAATTTAGTGC 960
QY 1297 CTTCCGTTGTAGCTTACCTTTGACCTTTCCTTTTATTCACAAATTAATTAATTAATTA 1356
    |||||||
Db 961 CTTCCGTTGTAGCTTACCTTTGACCTTTCCTTTTATTCACAAATTAATTAATTAATTA 1020
QY 1357 CTGAATTCACATTAATGCTATTTTAAAGTCAATTAATTAATTAATTAATTAATTAATTA 1416
    |||||||
Db 1021 CTGAATTCACATTAATGCTATTTTAAAGTCAATTAATTAATTAATTAATTAATTAATTA 1080
QY 1417 AGTAATGCTGTTGAATTTTGTATGTTTCCCAACATGCCCCCACTTGGATGTGGG 1476
    |||||||
Db 1081 AGTAATGCTGTTGAATTTTGTATGTTTCCCAACATGCCCCCACTTGGATGTGGG 1140
QY 1477 GTCAGGAGTTGAGTTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1536
    |||||||
Db 1141 GTCAGGAGTTGAGTTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1200
QY 1537 CAATGATATTCATTAATGTTGATGTTGACACAGAGGATTTTATCTGAGAAATACAC 1596
    |||||||
Db 1201 CAATGATATTCATTAATGTTGATGTTGACACAGAGGATTTTATCTGAGAAATACAC 1260
QY 1597 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1656
    |||||||
Db 1261 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
QY 1657 AATATGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1704
    |||||||
Db 1321 AATATGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1368

```

RESULT 9
 AA161016/c
 ID AA161016 standard; cDNA; 1799 BP.
 XX
 AA161016;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 5005.
 XX
 KW Human; neotropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20015312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0683036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HXSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR P-PSDB: AAM41860.

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

Claim 1: SEQ ID NO 5005; 10078bp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA158642-AA162213) with neurotrophic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

Sequence 1799 BP; 531 A; 389 C; 344 G; 535 T; 0 other:

Query Match 75.7%; Score 1295.4; DB 22; Length 1799;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 1401; Conservative 0; Mismatches 1; Indels 95; Gaps 1;

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QY 303 CCACGTGTCATGAAGAGCCAAAGGTGAGAGGCGCAAAAGGTGACCTGGGCGCTCGAG 362
DB 1799 CCACGTGTCATGAAGAGCCAAAGGTGAGAGGCGCAAAAGGTGACCTGGGCGCTCGAG 1740
QY 363 GGGAGGGGGGGGAGCATGGCCCCCAAGAGAGAGAGGGCTACCCGGGATCCACCCAGAAC 422
DB 1739 GGGAGGGGGGGGAGCATGGCCCCCAAGAGAGAGAGGGCTACCCGGGATCCACCCAGAAC 1680
QY 423 TT----- 424
DB 1679 TTGAGGCTGGAGTGCAGTGTGATCTTGGCTACCTGCACCTCCACCAAGGTTCAGC 1620
QY 425 -----CAGATTGCATTATGGCTTCT 447
DB 1619 GATTCTTGGCTCAACCTCTGGAGTAGCTGGGATTACAGATTGCAATTGCTGCTCTCT 1560
QY 448 GGAACCCACTTTCAGCAATTCAGAACAGTGGGATTATCTTACAGAGTTTACAGCAACAT 507
DB 1559 GGAACCCACTTTCAGCAATTCAGAACAGTGGGATTATCTTACAGAGTTTACAGCAACAT 1500
QY 508 TGGAACTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
DB 1499 TGGAACTTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 568 CTTTACCTTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627
DB 1439 CTTTACCTTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 628 CAATGCAACACAGTCTTACAGCTGTACAGCTGTGAAGTGAAGGCAATACATACATC 687
DB 1379 CAATGCAACACAGTCTTACAGCTGTACAGCTGTGAAGTGAAGGCAATACATACATC 1320
QY 688 CAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
DB 1319 CAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 748 TGGCGCTTCACATGAGGAGCACCACAGCTTCTCACCTTTCAGAGATTCTGCTTTTGA 807
DB 1259 TGGCGCTTCACATGAGGAGCACCACAGCTTCTCACCTTTCAGAGATTCTGCTTTTGA 1200
QY 808 AACTAAGTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 867
DB 1199 AACTAAGTAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140

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QY 868 TTTGTACATCTGAGACATTAAGCTTGAGGCTTTTACATTGCTGTATTCAAAAATT 927
DB 1139 TTTGTACATCTGAGACATTAAGCTTGAGGCTTTTACATTGCTGTATTCAAAAATT 1080
QY 928 ATTGGTTGCAATGCTGTGACGCTACAGGATCCCAATATGTTGACATTTAGGGGCT 987
DB 1079 ATTGGTTGCAATGCTGTGACGCTACAGGATCCCAATATGTTGACATTTAGGGGCT 1020
QY 988 CAGAGATACACACACAAATATCTTTCAGATGACCTTGATTAATATACAGCATCT 1047
DB 1019 CAGAGATACACACACAAATATCTTTCAGATGACCTTGATTAATATACAGCATCT 960
QY 1048 TTATCACTTCTTCTTGGCACTTAAAGATATTTCTCTGACGAGGTTGCAATATT 1107
DB 959 TTATCACTTCTTCTTGGCACTTAAAGATATTTCTCTGACGAGGTTGCAATATT 900
QY 1108 TTTTTCATACAGAGATCTTTGCAAGATTTTGACTCTGCTGCTTAAATTAATAC 1167
DB 899 TTTTTCATACAGAGATCTTTGCAAGATTTTGACTCTGCTGCTTAAATTAATAC 840
QY 1168 CAGTTTTCAGAACCCCTGAAGTTTAAAGTTCATTTATTTTAAACATTTGAGAGATC 1227
DB 839 CAGTTTTCAGAACCCCTGAAGTTTAAAGTTCATTTATTTTAAACATTTGAGAGATC 780
QY 1228 GGATGTAGTATATGACAGGCTGGGGCAAGAACAGGGGCTACCTGCTTATACCTA 1287
DB 779 GGATGTAGTATATGACAGGCTGGGGCAAGAACAGGGGCTACCTGCTTATACCTA 720
QY 1288 ATTATAGCCCTCCGTTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTAC 1347
DB 719 ATTATAGCCCTCCGTTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTAC 660
QY 1348 ATTAAACTCTGAATTCATACATACATATCTTAAAGTCAATAGATTTAGCTATTAAG 1407
DB 659 ATTAAACTCTGAATTCATACATACATATCTTAAAGTCAATAGATTTAGCTATTAAG 600
QY 1408 TGCTTGAACAGTATGTTGTTGTAATTTGTATGTTTCCCAACATCGCCCCCACTTC 1467
DB 599 TGCTTGAACAGTATGTTGTTGTAATTTGTATGTTTCCCAACATCGCCCCCACTTC 540
QY 1468 GGATGTGGGCTGACGAGGTTGAGGTTACATTAACAAAGTCAATATATCTATAGAG 1527
DB 539 GGATGTGGGCTGACGAGGTTGAGGTTACATTAACAAAGTCAATATATCTATAGAG 480
QY 1528 GTACAGTGCCCAATGATATTCAAATGTTGCATGTTGACAGAGGATTTATATCTGAAG 1587
DB 479 GTACAGTGCCCAATGATATTCAAATGTTGCATGTTGACAGAGGATTTATATCTGAAG 420
QY 1588 AACATACATTAATTAATTAATACCTTAGAGAAAGATTTTGAACCTTGTAGATTAAC 1647
DB 419 AACATACATTAATTAATTAATACCTTAGAGAAAGATTTTGAACCTTGTAGATTAAC 360
QY 1648 TGGCAACAAAATTAATGAGCAATATATGAAATTAACACACCTTGTAAAGATA 1704
DB 359 TGGCAACAAAATTAATGAGCAATATATGAAATTAACACACCTTGTAAAGATA 303

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RESULT 10
AA157798 standard; DNM: 810 BP.
ID AA157798: AAF94076;
AC AAF94076;
DT 23-MAY-2001 (first entry)
XX
XX
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 510.
XX
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KM rheumatoid arthritis; diabetes; PCR primer; ss.
XX
OS Synthetic.
XX
PN EP1067182-A2.


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XX 10-JAN-2001.
PD
XX
XX 07-JUL-2000; 2000EP-0114090.
XX
XX 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI; 2001-093989/11.
DR
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -
XX
XX Claim 4; SEQ ID 510; 609pp + CD ROM; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by
XX AAB88317 - AAB88419. Included in the invention are primers
XX AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
XX cDNA sequences of the invention. The invention also includes methods for
XX the production of antibodies directed against the proteins, and cDNA
XX sequences, which can be used in vaccines. The polynucleotide sequences
XX can be used in gene therapy. The polynucleotide sequences and the
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with inappropriate secretory
XX protein/membrane protein expression. The nucleic acids and complementary
XX sequences may also be used as DNA probes in diagnostic assays
XX (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
XX presence of similar nucleic acid sequences in samples. They may also be
XX used to study the expression and function of secretory proteins/membrane
XX polypeptides and their role in metabolism. The polypeptides may be used
XX as antigens in the production of antibodies against them and in assays to
XX identify modulators (agonists and antagonists) of expression and
XX activity. The antibodies and antagonists may also be used as therapeutic
XX agents to down regulate expression and activity. The antibodies may also
XX be used as diagnostic agents for detecting the presence of the
XX polypeptides in samples (e.g. by enzyme linked immunosorbant assay
XX (ELISA)). Examples of diseases which may be treated include rheumatoid
XX arthritis and diabetes.
XX
XX
XX Sequence 810 BP; 200 A; 201 C; 218 G; 188 T; 3 other:
SQ
Query Match 44.8%; Score 766.6; DB 22; Length 810;
Best Local Similarity 98.9%; Pred. No. 1.3e-212;
Matches 791; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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DB 313 AGCCATGCTCATGAAAGGACCAAGGTGAGAGGGCCGACCAAGGTGACCTGGGCTTCG 372
QY 361 AGGGAGCGGGGGGAGCATGGCCCCCAAGAGAGAGAGGGCTACCCGGGATTCCACAGA 420
DB 373 AGGGAGCGGGGGGAGCATGGCCCCCAAGAGAGAGAGGGCTACCCGGGATTCCACAGA 432
QY 421 ACTTCAGATTCATTCATGAGCTTCTCTGAGCAACCCACCTTCACATTCAGAAAGGGGAT 480
DB 433 ACTTCAGATTCATTCATGAGCTTCTCTGAGCAACCCACCTTCACATTCAGAAAGGGGAT 492
QY 481 TATCTTCAGAGTGTGAGAGCAACATTCGAAGTCTTGTGATGATGACTGTAGATT 540
DB 493 TATCTTCAGAGTGTGAGAGCAACATTCGAAGTCTTGTGATGATGACTGTAGATT 552
QY 541 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCACATGATGAAAGCATGAGATGT 600
DB 553 TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCACATGATGAAAGCATGAGATGT 612
QY 601 TGAGGAAGTGTATGTCTACCTTATGACACATGGAACACAGTCTTCAGATGTACAGCTA 660
DB 613 TGAGGAAGTGTATGTCTACCTTATGACACATGGAACACAGTCTTCAGATGTACAGCTA 672
QY 661 TGAATGAAAGGCAATCAGATACATCCAGCAATCATGCTGTGAGTGAAGTGAAGCAAGG 720
DB 673 TGAATGAAAGGCAATCAGATACATCCAGCAATCATGCTGTGAGTGAAGTGAAGCAAGG 731
QY 721 GGATGAGTTGGCTGCGAATGAGGCAATGGCGCTCTCCATGGGGACCAACCAAGCTTCTC 780
DB 722 GGATGAGTTGGCTGCGAATGAGGCAATGGCGCTCTCCATGGGGACCAACCAAGCTTCTC 790
QY 781 CACCTTTCAGAGATTCCTTCG 800
DB 791 CACCTTTCAGAGATTCCTTCG 810

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RESULT 11
ID ABR35591 standard; DNA: 741 BP.
XX ABR35591;
AC 08-MAY-2002 (first entry)
XX
DE Gene encoding novel human secreted or membrane-associated protein #10.
XX
KW Human; secreted protein; membrane-associated protein; hypertension;
KW inflammatory disorder; neurological disorder; haematopoietic disorder;
KW skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW neurodegenerative disorder; nervous system disorder; bacterial infection;
KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW hypotension; sexual development disorder; blood disorder; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200204600-A2.
PD 17-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-US21985.
XX
PR 12-JUL-2000; 2000US-218033P.
PR 21-AUG-2000; 2000US-226517P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agrawal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
PI Smith RF, Xiang Z, Xie Q;
XX WPI; 2002-188468/24.
XX P-PSDB: AAB84371.
XX

PT Novel secreted and membrane-associated polypeptides and polynucleotides
 PT encoding the polypeptides, for preventing, treating and ameliorating
 PT cancers, mental or sexual developmental disorders, and malignant tumours
 XX
 PS Claim 2: Page 106; 151pp; English.
 XX
 CC The present invention relates to the isolation of novel human secreted
 CC or membrane-associated proteins and the genes encoding them. The
 CC sequences of the invention are useful for treating, preventing and
 CC ameliorating various diseases such as inflammatory disorders (e.g.
 CC asthma), neurological disorders (e.g. dementia), hematopoietic
 CC disorders, skeletal developmental disorders, growth abnormalities,
 CC neurodegenerative disorders (e.g. Huntington's disease), nervous system
 CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),
 CC peripheral myelinopathies, viral and bacterial infections,
 CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
 CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,
 CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental
 CC or sexual development disorders, and dysfunctions of the blood cascade
 CC system including those leading to stroke. ABK3582-ABK35609 represent
 CC the genes encoding the novel human secreted or membrane-associated
 CC proteins of the invention.
 XX
 SQ Sequence 741 BP; 191 A; 178 C; 200 G; 172 T; 0 other;

Query Match 43.3%; Score 741; DB 24; Length 741;

Best Local Similarity 100.0%; Pred. No. 3.7e-205; Mismatches 0; Indels 0; Gaps 0;

Matches 741; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 ATGCTTTGAGGAGCGCTCATCTATTGGCAACTGCTGCTTTGTTTCCCTCTTCTTTCG 136
 DB 1 ATGCTTTGAGGAGCGCTCATCTATTGGCAACTGCTGCTTTGTTTCCCTCTTTCG 60
 QY 137 CTGTGCAAGATGATACATGAGTCTCCAAACCGGAGACTACCCCAAGCTGACGT 196
 DB 61 CTGTGCAAGATGATACATGAGTCTCCAAACCGGAGACTACCCCAAGCTGACGT 120
 QY 197 AAGTGTTCATGAGACATACAGCTTTGAGGCTACCAAGGCGCCCTGGGACCGGGG 256
 DB 121 AAGTGTTCATGAGACATACAGCTTTGAGGCTACCAAGGCGCCCTGGGACCGGGG 180
 QY 257 CCTCTGGGATTCAGAGAAACCATGGAACATGGAACATGAGCCACTGCTCATGAA 316
 DB 181 CCTCTGGGATTCAGAGAAACCATGGAACATGGAACATGAGCCACTGCTCATGAA 240
 QY 317 GAGGCCAAAGGTGAGAGAGGCGCAAGGTGACCTGGGCTTGAGGGGAGCGGGGAG 376
 DB 241 GAGGCCAAAGGTGAGAGAGGCGCAAGGTGACCTGGGCTTGAGGGGAGCGGGGAG 300
 QY 377 CATGGGCCCAAGAGAGAGAGGCTACCGGGGATTCACACAGACTTCGATTGCAATTC 436
 DB 301 CATGGGCCCAAGAGAGAGAGGCTACCGGGGATTCACACAGACTTCGATTGCAATTC 360
 QY 437 ATGGCTTCTCTGCAACCCACTTCAGCAATCAGAACAGTGGATTATCTTCACAGAGTT 496
 DB 361 ATGGCTTCTCTGCAACCCACTTCAGCAATCAGAACAGTGGATTATCTTCACAGAGTT 420
 QY 497 GAGACCAACATTTGGAACCTTTGATGATACATGATGATGATTTGGGGCCCAAGATCA 556
 DB 421 GAGACCAACATTTGGAACCTTTGATGATACATGATGATGATTTGGGGCCCAAGATCA 480
 QY 557 GGTGTGATTTCTTCACCTTCAGCATGATGATGATGATGATTTGGAAGGTATGTTG 616
 DB 481 GGTGTGATTTCTTCACCTTCAGCATGATGATGATGATTTGGAAGGTATGTTG 540
 QY 617 TACCTTATGCAATGAGCAACAGCTTCAGCATGATGATGATGATGATGATGATGAT 676
 DB 541 TACCTTATGCAATGAGCAACAGCTTCAGCATGATGATGATGATGATGATGATGAT 600
 QY 677 TCAGATATACATCCAGCATATGCTGTCTGATGATGATGATGATGATGATGATGATG 736
 DB 601 TCAGATATACATCCAGCATATGCTGTCTGATGATGATGATGATGATGATGATGATG 660

QY 737 CGAATGGGCAATGAGCGCTCTCCATGAGGACCAACAGCTTCTCCACCTTTGAGATTC 796
 DB 661 CGAATGGGCAATGAGCGCTCTCCATGAGGACCAACAGCTTCTCCACCTTTGAGATTC 720
 QY 797 CTGCTCTTTGAACATAGTAA 817
 DB 721 CTGCTCTTTGAACATAGTAA 741

RESULT 12

AAC9776
 ID AAC9776 standard; cDNA; 1035 BP.

XX AAC9776;

DT 08-MAR-2001 (first entry)

DE Skin cell cDNA, SEQ ID NO: 424.

XX Rat; skin cell; cytosolic; anti-inflammatory; anti-HIV;

KW neotropic; neuroprotective; vulnery; immunomodulatory; vaccine;

KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;

XX Inflammation; neurological disease; ss.

OS Rattus sp.

PN MO200069884-A2.

XX 15-MAY-2000; 2000MO-N200075.

XX 14-MAY-1999; 99US-0312283.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

DR WPI: 2001-007495/01.

XX P-PSDB; AAB55908.

PS New isolated polynucleotide used in the identification of genetic

PT disorders and encoding polypeptides used for treating inflammatory

XX disease, cancer and neurological diseases -

XX Claim 1; Page 317-318; 352pp; English.

XX The present polynucleotide encodes a polypeptide which is expressed in

CC mammalian skin cells. The polypeptide is useful for stimulating

CC keratinocyte growth and motility, inhibiting the growth of cancer cells,

CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of

CC tumours, modulating skin inflammation, stimulating the growth of

CC epithelial cells, inhibiting the binding of human immunodeficiency virus

CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and

CC neurological diseases. The polynucleotide can be used as a marker, in

CC the identification of genetic disorders, and for the design of

XX oligonucleotides for examining expression patterns.

SQ Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;

Query Match 40.7%; Score 696.2; DB 22; Length 1035;

Best Local Similarity 82.8%; Pred. No. 5.1e-192; Mismatches 168; Indels 2; Gaps 2;

Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;

QY 33 CTCTGCTGCTCTTCAGGAGACTGTGAGGCTGTTGAGATATGCTTTGAGGAGGAGC 92
 DB 48 CCGATTCAGCTTCCCGGAGAGATTCGCGATTGTCACGAGCATGCTCAGGAGGAGC 107
 QY 93 TCATCTATGCACTGCTGCTGCTTTGTTTCCCTCCCTTTGCTGCTGCTGCTGCTGCTG 152
 DB 108 TCCTGTGTGACACCTGCTGCTTTGCTTTCTCCCTTTGCTGCTGCTGCTGCTGCTG 167

OY 153 ACATGAGTCTCCAAACCGGAGACTACCCGAGCTGCAATGAGTGTTCATGAG 212
 |||||
 Db 168 ACATGAGTCTCCAAACCGGAGACTACCCGAGCTGCAATGAGTGTTCATGAG 227
 |||||
 OY 213 ACTAGAGTCTCCAAACCGGAGACTACCCGAGCTGCAATGAGTGTTCATGAG 272
 |||||
 Db 228 ATATGAGTCTCCAAACCGGAGACTACCCGAGCTGCAATGAGTGTTCATGAG 287
 |||||
 OY 273 GAAACCATGGAACAAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 332
 |||||
 Db 288 GAAACCATGGAACAAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 347
 |||||
 OY 333 AGGCGCAAAAGGTGAGTGGGGCTGAGGGGAGCGGGGAGAGTGGGGCAAGAG 392
 |||||
 Db 348 AAGAGGACAAAGGAGGAGTGGGGCTGAGGGGAGCGGGGAGAGTGGGGCAAGAG 407
 |||||
 OY 393 AGAAGGCTACCCGGGAGTTCACCAAGAACTTCAAGATTGATTCGCTTCGCA 452
 |||||
 Db 408 AGAAGGATACCCGAGGGGTGCGCAGAGCTGCAAGATTGCTTCATGCTTCAGCA 467
 |||||
 OY 453 CCCACTTCAGCAATCAGAACAGTGGGATTCCTCAGCAGTGTTCAGCAATGGA 512
 |||||
 Db 468 CTCACCTTCAGCAATCAGAACAGTGGGATTCCTCAGCAGTGTTCAGCAATGGA 527
 |||||
 OY 513 ACTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 572
 |||||
 Db 528 ACTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587
 |||||
 OY 573 CTTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 632
 |||||
 Db 588 CTTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 647
 |||||
 OY 633 GCAACACAGTCTTCAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAG 692
 |||||
 Db 648 GTAACAGGTTCTTCAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAG 707
 |||||
 OY 693 ATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 752
 |||||
 Db 708 ACCTTCAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 767
 |||||
 OY 753 CTTTCAGTGGGAGCACCAAGCGTTCCTCAGATTCCTGCTTCCTTCGAACTA 812
 |||||
 Db 768 CTTTCAGTGGGAGCACCAAGCGTTCCTCAGATTCCTGCTTCCTTCGAACTA 827
 |||||
 OY 813 AGTAAATATAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 871
 |||||
 Db 828 AGTAAATATAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 887
 |||||
 OY 872 TTACGATCTGGAACATTAAGTTGAGGTTTACATTCCTGATTCGAAATATATG 931
 |||||
 Db 888 TTACGATCTGGAACATTAAGTTGAGGTTTACATTCCTGATTCGAAATATATG 946
 |||||
 OY 932 GTTTCAGTCTGGAACATTAAGTTGAGGTTTACATTCCTGATTCGAAATATATG 991
 |||||
 Db 947 GTTTCAGTCTGGAACATTAAGTTGAGGTTTACATTCCTGATTCGAAATATATG 1006
 |||||
 OY 992 AGATCAACCAAAATAGTCTTCAGA 1020
 |||||
 Db 1007 AGATCAACCAAAATAGTCTTCAGA 1035
 |||||

RESULT 13

ABL34928

ID ABL34928 standard; cDNA: 1035 BP.

AC ABL34928;

XX 04-APR-2002 (first entry)

XX Rat cDNA isolated from skin cells SEQ ID NO: 424.

XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;

XX developmental defect; inflammatory disease; dermatological; vulnary;

KW

KM

IMMUNOMODULATOR; anti-inflammatory; cytostatic; neuroprotective; gene;

SS.

Rattus sp.

MO200190357-A1.

KM Immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
 KW SS.
 XX Rattus sp.
 OS MO200190357-A1.
 PN 29-NOV-2001.
 XX 24-MAY-2001; 2001WO-N200099.
 XX 24-MAY-2000; 2000US-20650P.
 PR 25-JUL-2000; 2000US-221232P.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA Watson JD, Strachan L, Sleeman M, Onrust R, Murlison JG, Kumble KD;
 PI WPI; 2002-122020/16.
 DR
 XX
 PT New polynucleotides and polypeptides encoded by the polynucleotides
 PT isolated from skin cells, useful for treating skin wounds, cancers,
 PT growth and developmental defects, inflammatory diseases, or for
 PT modulating immune responses
 PS Claim 1; Page 262; 466pp; English.
 XX
 CC The present invention provides the protein and coding sequences of cDNAs
 CC isolated from human, murine and rat skin cell libraries. The sequences
 CC can be used in the development of therapeutic agents useful in the
 CC treatment of skin diseases, including skin wounds, cancer, growth
 CC defects, developmental defects and inflammatory diseases. The proteins
 CC have important roles in the induction of hair growth, cell proliferation
 CC and cell-cell interaction, in maintaining tissue integrity, in wound
 CC healing and in modulating immune responses. The present sequence is a
 CC cDNA of the invention.
 CC
 XX
 SQ Sequence 1035 BP; 255 A; 242 C; 298 G; 240 T; 0 other;

Query Match 40.7%; Score 696.2; DB 24; Length 1035;
 Best Local Similarity 82.8%; Pred. No. 5.1e-192;
 Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;

OY 33 CTCGCTCTCTTCAGGAGACATCTGAGGCTGTGATGATGATGATGATGATGAT 92
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 Db 48 CCCATCAGCTTCCCGGGGAGATTCTGCCGATTGTCAGAGCCATGCTCAGAGGCGAGC 107
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 OY 93 TCATCTATTTGGCACTGCTGCTTTGTTTCTCCCTTTTGGCTGTGCAAGTGAAT 152
 |||||
 Db 108 TCGCTCTGGTGCACCTGCTGCTTTGCTTCTTCCTCATTGCTGTGCTGATGATGAT 167
 |||||
 OY 153 ACATGAGTCTCCAAACCGGAGACTACCCGAGCTGAGTGAATGTTGATGAGAG 212
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 Db 168 ACATGAGTCTCCAAACCGGAGACTACCCGAGCTGAGTGAATGTTGATGAGAG 227
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 OY 213 ACTAGAGTCTCCAAACCGGAGACTACCCGAGCTGAGTGAATGTTGATGAGAG 272
 |||||
 Db 228 ATATGATTCCTGTTTACCAAGGGCCCTTGAGCCCTCCAGGCTCTGCAATTCAG 287
 |||||
 OY 273 GAAACCATGGAACAAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAG 332
 |||||
 Db 288 GAAACCATGGAACAAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAG 347
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 OY 333 AGGCGCAAAAGGTGAGTGGGGCTGAGGGGAGCGGGGAGAGTGGGGCAAGAG 392
 |||||
 Db 348 AAGAGGACAAAGGAGGAGTGGGGCTGAGGGGAGCGGGGAGAGTGGGGCAAGAG 407
 |||||
 OY 393 AGAAGGCTACCCGGGAGTTCACCAAGAACTTCAAGATTGATTCGCTTCGCA 452
 |||||
 Db 408 AGAAGGATACCCGAGGGGTGCGCAGAGCTGCAAGATTGCTTCATGCTTCAGCA 467
 |||||
 OY 453 CCCACTTCAGCAATCAGAACAGTGGGATTCCTCAGCAGTGTTCAGCAATGGA 512
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Db 468 CTCACCTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTGAGCAACCAATTGGAA 527
QY 513 ACTCTTTGATGTCATGCTGGTATGTTGGGGCCCAAGTATCAGGTATCTTATCTTCA 572
Db 528 ACTCTTGATGATGCTAGTACTGTAGATTTGGGCCCCCGATACAGGCGTGTATTTCTTCA 587
QY 573 CCTTCAGCATGATGAAGCATGAGATGTTGAGGAAGTATGTATGCTTATATGCACAATG 632
Db 588 CCTTCAGCATGATGAAGCATGAGATGTTGAGGAAGTATGTATGCTTATATGCACAATG 647
QY 633 GCACACAGTCTTTCAGCATGTACAGCTATGAAATGAAGGGCAATACATACATCCAGCA 692
Db 648 GTAAACAGGTGTTACAGCATGTACACCTATGAACAAAGGAAATACATACATCCAGCA 707
QY 693 ATCATGCTGTGCTGAAGTACAGCAAGGAGATGAGTGTGCTGCGTGAAGGCAATGGG 752
Db 708 ACCATGACAGTGTGATGTTGGCCAAAGATGATGATGCTGCTAAGAAATGGCAACGGTG 767
QY 753 CTCTCCATGGGAGCACCACCAAGCTTCTCCACCTTTCAGAGATTCCTGCTTTTGAACCTA 812
Db 768 CCTTCATGGGGAGCACCAGCGCTTCTTACTCTGCAAGGCTTCTGCTTTTGAACCTA 827
QY 813 ACTAATATATGACTAGATAGCTCCACTTGGGGAAGACTTGTAGCTGAGCT-GATTGG 871
Db 828 AGTATGAGGAAGTACAGTACTCCATGCTAAGGCGCATTTGTAGTGAAGCTAGAGCTTG 887
QY 872 TTACATCTCGAGCAACATTAAAGTGTGAGGCTTTTACATTTGCTGATTCGTAACAAATTAATG 931
Db 888 TTAGATGTGAGAGGCTGTGGAGTTG-GGCTTCTATGAGTATTTAAGTCTTTACATTTG 946
QY 932 GTTCAGATGTTGTCACGCTACAGGTACACCAATATGTTGACAAATTCAGGGCTCAGA 991
Db 947 GTACACAGTCTCTCATTTCTATATGCAATACCAATATATGATGATCTTTAGGGCTAGGA 1006
QY 992 AGAATCAACCAAAATAGCTTCTCAGA 1020
Db 1007 AGAATGACCAACAGTAAATATTTCCAGA 1035

RESULT 14
AAZ61633
ID AAZ61633 standard: cDNA: 1123 BP.
AC AAZ61633;
XX
DT 27-MAR-2000 (first entry)
XX
DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:28.
XX
KM Skin: dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KM embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KM secreted; transmembrane; inflammation; cancer; neurological disease;
KM angiogenesis; tumour vascularisation; growth disorder;
KM developmental disorder; skin wound; hair follicle disorder;
KM anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
XX
OS Rattus sp.
XX
PN W09955865-A1.
XX
PD 04-NOV-1999.
XX
PE 29-APR-1999; 99WO-NZ00051.
XX
PR 29-APR-1998; 98US-0069726.
XX
PR 09-NOV-1998; 98US-0188930.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
XX
DR WPI, 2000-072177/06.
XX

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PT Novel polynucleotides useful for the treatment of various conditions
PT including wounds and cancer
PS Claim 1, Page 73: 235pp: English.
XX
CC The invention relates to novel nucleic acid sequences derived from rat
CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC cells. Polypeptides of the invention may be used to treat inflammation,
CC cancer and neurological diseases. The proteins may be used to stimulate
CC the growth and motility of keratinocytes, to inhibit the growth of
CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC modulate skin inflammation, to modulate epithelial cell growth and to
CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC to treat growth and developmental defects, skin wounds and hair follicle
CC disorders. Sequences AAZ61606-261832 represent cDNA sequences derived
CC from several mouse, rat or human skin cell types. Sequences
CC AAZ61606-261649, AAZ61725-261765, AAZ61802-261811 and AAZ61826 encode
CC proteins with an N-terminal signal sequence, indicating that the proteins
CC are secreted. Sequences AAZ61650-261668, AAZ61766-261780, AAZ61812-261817
CC and AAZ61827-261829 encode proteins with one or more putative
CC transmembrane domains.
XX
SQ Sequence 1123 BP: 277 A: 266 C: 321 G: 258 T: 1 other:
XX
Query Match 40.7%; Score 696.2; DB 21; Length 1123;
Best Local Similarity 82.8%; Pred. No. 5,3e-192;
Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;
QY 33 CTCTGCTGCTCTTCTCAGGAGACTGTGAGCTCTGTTGAATCATGCTTTGGAGGCAGC 92
Db 136 CCCATCAGCTTCCCGGGAGAGATTCGCGATTTGTCACAGCAAGCTCAGAGGCACAC 195
QY 93 TCATCTATGCGAATCGTGGCTTTGTTTCTCCCTTTTGGCCGTGCAAGATGAAT 152
Db 196 TCGTCTGGGAGACCTGCTGCTGCTTCTTCTCCATTTGCTGCTGTCAGATGAAT 255
QY 153 ACATGAGTCTCCACAAACCGGAGAGACTACCCCAAGACTGACGTAAGTGTTCATGAG 212
Db 256 ACATGAGTCTCCACAAAGCTGAGAGAGCTGCCCAAGACTGACGTAAGTGTTCATGAG 315
QY 213 ACTACAGCTTTGAGGCTACCAAGGCCCTCGGACCCAGCCCTCTGGCATTCAG 272
Db 316 ATTATGATTTCCGTGTGTACCAAGGGCCCTGAGACCCCAAGCTCTCTGGCATTCAG 375
QY 273 GAACCATGGAACATGGCAACATGAGAGCCACTGCTGATGAGGAGCAAAAGTGAGA 332
Db 376 GAACCATGGAACATGGAATTAACGAGCCACTGCGACGAGAGGGCCAAAGGGTGAGA 435
QY 333 AGGCGACAAAGGTGACCTGGGGCTCGAGGGAGCGGGGCGCAGATGGCCCCCAAGAG 392
Db 436 AAGGACACAAAGGCACTGGGGCCCTCGAGGGGAACGGGGGCAAGTGGCCCCCAAGAG 495
QY 393 AGAAGGCTACCCGGGGATTCACACGAACTTCAGATTCATTCATGCTTCTGCGAA 452
Db 496 AGAAGGATACCCAGGGGCTGCCACAGACCTGAGATTCGTTCAAGCTTCTCTAGCGA 555
QY 453 CCCACTTCAGCAATCAGACAGTGGGATTTCTTCGACATGGTTGAGACCAACATTGGAA 512
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Db 616 ACTTCTTATGTCATGATGATGATGATTTGGGCCCCCAGTATCAGTGTATTTCTTCA 675
QY 573 CCTTCAGCATGATGAAGCATGAGATGTTGAGGAAGTATGTATGCTTATATGCACAATG 632
Db 676 CCTTCAGCATGATGAAGCATGAGATGTTGAGGAAGTATGTATGCTTATATGCACAATG 735
QY 633 GCACACAGTCTTTCAGCATGTACAGCTATGAAATGAAGGGCAATACATACATCCAGCA 692
Db 736 GTACACAGGTGTTACAGCATGTACAGTATGAACAAAGGAAATACATACATCCAGCA 795

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Db 976 TTAGGATCTAGGGGCTGTGAGFTG-GGCTTCCTATGAGATATTAACTGTTACATTG 1034
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Db 1035 GTCACACTGCTACTCATCTTAATGCAATACCAATTATGTTGACTTTAGGGGCTAGCA 1094
QY 992 AGATCAACCAACAATAATAGTCTTCTCAGA 1020
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Search completed: January 15, 2003, 17:41:35
Job time : 362 secs

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PRIOR APPLICATION NUMBER: PCT/US00/34956

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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 1
LENGTH: 1712
TYPE: DNA
ORGANISM: Homo Sapien
us-10-036-041-1

Query Match 100.0%; Score 1712; DB 9; Length 1712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGCATCTGCCGAGAGACACGCTCTGGAGCTCTGCTCTTCTGAGGAGACTCTGA 60
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1 GGCATCTGCCGAGAGACACGCTCTGGAGCTCTGCTCTTCTGAGGAGACTCTGA 60
61 GGCCTGTGGAGATCATGCTTTGGAGGACGCTCATTTGSCAACTGCTGGCTTGT 120
|||||
61 GGCCTGTGGAGATCATGCTTTGGAGGACGCTCATTTGSCAACTGCTGGCTTGT 120
121 TTTCCTCCCTTTTGGCTGTCAAGATGATACATGAGCTCCACAACTGGAGACT 180
|||||
121 TTTCCTCCCTTTTGGCTGTCAAGATGATACATGAGCTCCACAACTGGAGACT 180
181 ACCCCAGACTGAGTGAAGTGTGTGATGAGACTACAGCTTTGAGGCTACCAAGGCC 240
|||||
181 ACCCCAGACTGAGTGAAGTGTGTGATGAGACTACAGCTTTGAGGCTACCAAGGCC 240
241 CCTGGGCCACCGGGCCCTCTGCTGATTCAGAAACCATGGAACAATGGCAATGG 300
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241 CCTGGGCCACCGGGCCCTCTGCTGATTCAGAAACCATGGAACAATGGCAATGG 300
301 AGCCACGTGTCATGAAGAGCCAAAGTGAGAGAGGCGACAAAGTGAACCTGGGCTCG 360
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301 AGCCACGTGTCATGAAGAGCCAAAGTGAGAGAGGCGACAAAGTGAACCTGGGCTCG 360
361 AGGAGACGGGGGCGAGCATGGCCCCAAAGAGAGAGGGCTACCCGGGGATTCCACCGA 420
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361 AGGAGACGGGGGCGAGCATGGCCCCAAAGAGAGAGGGCTACCCGGGGATTCCACCGA 420
421 ACTTCAGATTGATTCATGAGCTTCTGCAACCCACTTCAGCAATCAGAAAGTGGAT 480
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421 ACTTCAGATTGATTCATGAGCTTCTGCAACCCACTTCAGCAATCAGAAAGTGGAT 480
481 TATCTCAGAGCTGTGAGCAACCAATTTGGAACCTCTTGTATGATCATGAGTGTAGAT 540
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661 TGAATGAAGGCAATCAGATACATCCAGCAATCATGCTGTGAGAGGCAAGG 720
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661 TGAATGAAGGCAATCAGATACATCCAGCAATCATGCTGTGAGAGGCAAGG 720
721 GGATGAGTTTGGCTGGCAATGGCAATGGGCTCTCCATGGGAGCAACCAAGCTTCTC 780
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721 GGATGAGTTTGGCTGGCAATGGGCTCTCCATGGGAGCAACCAAGCTTCTC 780

QY 781 CACCTTGCAGATTCCTGCTCTTTGAACTAAGTAATATAGTAGAATAGCTCCAC 840
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Db 781 CACCTTGCAGATTCCTGCTCTTTGAACTAAGTAATATAGTAGAATAGCTCCAC 840
QY 841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTACATCTGAGGAACATTAAGTTGAG 900
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Db 841 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTACATCTGAGGAACATTAAGTTGAG 900
QY 901 GTTTACATGCTGATTAATAAATAATTTGTGCAATGTTGTCAGCTCAGCTTACA 960
|||||
Db 901 GTTTACATGCTGATTAATAAATAATTTGTGCAATGTTGTCAGCTCAGCTTACA 960
QY 961 CCAATATGTTGACAAATTCAGGGGCTCAGAGAATCAACCAAAATAGTCTTCAGA 1020
|||||
Db 961 CCAATATGTTGACAAATTCAGGGGCTCAGAGAATCAACCAAAATAGTCTTCAGA 1020
QY 1021 TGAACCTGACATATATCTGACATCTTTATCTCTTCTGTCAGCTTAAAGATTAAT 1080
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Db 1021 TGAACCTGACATATATCTGACATCTTTATCTCTTCTGTCAGCTTAAAGATTAAT 1080
QY 1081 TCTGCTGACGAGGTTGGAATATTTTCTATCAGAGAAGTATTCAGAAAGATTT 1140
|||||
Db 1081 TCTGCTGACGAGGTTGGAATATTTTCTATCAGAGAAGTATTCAGAAAGATTT 1140
QY 1141 TTGACTACTGCTTTTATTAATACAGTTTTCAGAAACCCCTGAAGTTTAAGTTCA 1200
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Db 1141 TTGACTACTGCTTTTATTAATACAGTTTTCAGAAACCCCTGAAGTTTAAGTTCA 1200
QY 1201 TTAATCTTTATTAATTTGAGAAATCGAGTATGATATGACAGAGGCTGGGGCAAGA 1260
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Db 1201 TTAATCTTTATTAATTTGAGAAATCGAGTATGATATGACAGAGGCTGGGGCAAGA 1260
QY 1261 CAGGGGCACTAGCTGCTTATAGCAATTTAGTGGCCCGGTTGACCTTACCTTTG 1320
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Db 1261 CAGGGGCACTAGCTGCTTATAGCAATTTAGTGGCCCGGTTGACCTTACCTTTG 1320
QY 1321 ACCCTTCTTTGATCCCAAAATACATTAAGCTGTAATTCACATCAATGCTATTT 1380
|||||
Db 1321 ACCCTTCTTTGATCCCAAAATACATTAAGCTGTAATTCACATCAATGCTATTT 1380
QY 1381 TAAAGTCAATATTTTACCTATTAAGTCTTGACCAAGTAATGCTGTTAATTTTGTG 1440
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Db 1381 TAAAGTCAATATTTTACCTATTAAGTCTTGACCAAGTAATGCTGTTAATTTTGTG 1440
QY 1441 ATGTCCTCCCATGCGCCCAACTCGAGTGGGGGTAGAGAGTGGAGTGCATATT 1500
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Db 1441 ATGTCCTCCCATGCGCCCAACTCGAGTGGGGGTAGAGAGTGGAGTGCATATT 1500
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Db 1501 AACCAATGTCATTAATATCTCATAGAGTACAGTGCATATTCATTAATGTTGCATG 1560
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QY 1621 ATTTGCACTGCTTATTAATAAAGTGGCAAGAAATGTAATAGCAATATATGGA 1680
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Db 1621 ATTTGCACTGCTTATTAATAAAGTGGCAAGAAATGTAATAGCAATATATGGA 1680
QY 1681 ATTAACACACCTTTGTTAAGATTAATAAATAA 1712
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Db 1681 ATTAACACACCTTTGTTAAGATTAATAAATAA 1712

RESULT 2
US-10-035-855-1
: Sequence 1, Application US/10035855
: Publication No. US20030008348A1
: GENERAL INFORMATION:
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.

APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Guirney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C4
CURRENT APPLICATION NUMBER: US/10/035, 855
CURRENT FILING DATE: 2001-12-26
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PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 1
LENGTH: 1712
TYPE: DNA
ORGANISM: Homo Saplen
US-10-035-855-1

Query Match 100.0%; Score 1712; DB 9; Length 1712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCATCTGCCGAGAGACCAAGCTCTGAGCTCTGCTCTTCTCAGGAGACTGGA 60
DB 1 GGCATCTGCCGAGAGACCAAGCTCTGAGCTCTGCTCTTCTCAGGAGACTGGA 60
QY 61 GGCCTCTGTGAGATCAATGCTTTGGAGGAGCTCATATATGGAACGCTGGCTTTGTT 120
DB 61 GGCCTCTGTGAGATCAATGCTTTGGAGGAGCTCATATATGGAACGCTGGCTTTGTT 120
QY 121 TTCTCTCTCTTTTCTCTGTCTCAAGATGATATACATGAGAGTCTCCACAAACGGAGACT 180
DB 121 TTCTCTCTCTTTTCTCTGTCTCAAGATGATATACATGAGAGTCTCCACAAACGGAGACT 180
QY 181 ACCCCAGACTGCAAGTATGTTGTCTATGAGACTACAGCTTTGAGAGCTACCAAGGCC 240
DB 181 ACCCCAGACTGCAAGTATGTTGTCTATGAGACTACAGCTTTGAGAGCTACCAAGGCC 240

QY 241 CCTTGGGCCACCGGGCCCTCTGCGATTCCAGAAACCTGGAACAATGCAACATG 300
DB 241 CCTTGGGCCACCGGGCCCTCTGCGATTCCAGAAACCTGGAACAATGCAACATG 300
QY 301 AGCCACTGTCTATGAAGAGCCAAAGGTGAGAGGGGACAAAGGTGACTGGGGCTCG 360
DB 301 AGCCACTGTCTATGAAGAGCCAAAGGTGAGAGGGGACAAAGGTGACTGGGGCTCG 360
QY 361 AGGGAGGGGGGGGAGAGTGGCCCAAGAGAGAGAGGGGTACCCGGGGATTCCACCA 420
DB 361 AGGGAGGGGGGGGAGAGTGGCCCAAGAGAGAGGGGTACCCGGGGATTCCACCA 420
QY 421 ACTTCAGATTGATTCATGAGCTTCTCTGCAACCACTTCAGCATGCAAGAGTGGAT 480
DB 421 ACTTCAGATTGATTCATGAGCTTCTCTGCAACCACTTCAGCATGCAAGAGTGGAT 480
QY 481 TATCTTCAGAGTGTGAGACCAACATTTGAACTCTTTGATGTCAATGAGTGTAGATT 540
DB 481 TATCTTCAGAGTGTGAGACCAACATTTGAACTCTTTGATGTCAATGAGTGTAGATT 540
QY 541 TGGGGCCCAAGTATCAGGTGTCTATTCTTCACTTCAGCATGATGAAGCATGAGATGT 600
DB 541 TGGGGCCCAAGTATCAGGTGTCTATTCTTCACTTCAGCATGATGAAGCATGAGATGT 600
QY 601 TGAGGAAGTGTATGTATCTTATGCAATGGAACAGAGCTTCACATGTATACGCTA 660
DB 601 TGAGGAAGTGTATGTATCTTATGCAATGGAACAGAGCTTCACATGTATACGCTA 660
QY 661 TGAATGAAGGCAAAATCAGATACATCCAGCAATCATCTGTGTAAGTGAACCAAG 720
DB 661 TGAATGAAGGCAAAATCAGATACATCCAGCAATCATCTGTGTAAGTGAACCAAG 720
QY 721 GGATGAGTGTGGCTGGCAATGGGCAATGGGCTCTCATGGGAGCCCAAGCTTCTC 780
DB 721 GGATGAGTGTGGCTGGCAATGGGCAATGGGCTCTCATGGGAGCCCAAGCTTCTC 780
QY 781 CACCTTGCAGAGATTCTGCTCTTGAAGTAAATATATGATGATAGCTGATCCAC 840
DB 781 CACCTTGCAGAGATTCTGCTCTTGAAGTAAATATATGATGATAGCTGATCCAC 840
QY 841 TTTGGGGAAGACTGTAGCTGAGCTGATTTGTAGCATGTGAGAACTTAAAGTTGAG 900
DB 841 TTTGGGGAAGACTGTAGCTGAGCTGATTTGTAGCATGTGAGAACTTAAAGTTGAG 900
QY 901 GTTTTACATCTCTGATTCACAAAATTTATGGTGGCAATGTTTTCACGCTACAG 960
DB 901 GTTTTACATCTCTGATTCACAAAATTTATGGTGGCAATGTTTTCACGCTACAG 960
QY 961 CCAATTAATGTGAGCAATTCAGGGGCTCAGAAATCAACCAAAATATAGTCTTCAGA 1020
DB 961 CCAATTAATGTGAGCAATTCAGGGGCTCAGAAATCAACCAAAATATAGTCTTCAGA 1020
QY 1021 TGACCTTGCAATATATCTCAGATCTTTATACATCTTTCTTGGCACCCTAAAGATAT 1080
DB 1021 TGACCTTGCAATATATCTCAGATCTTTATACATCTTTCTTGGCACCCTAAAGATAT 1080
QY 1081 TCTCTCTGAGAGCAGGTGGAATATTTTCTCTATCACAAGATCATTTGCAAGATTT 1140
DB 1081 TCTCTCTGAGAGCAGGTGGAATATTTTCTCTATCACAAGATCATTTGCAAGATTT 1140
QY 1141 TTGACTACTGTCTTTTATTTAATACAGTTTTCAGAACCCCTGAGSTTTTAAGTTCA 1200
DB 1141 TTGACTACTGTCTTTTATTTAATACAGTTTTCAGAACCCCTGAGSTTTTAAGTTCA 1200
QY 1201 TTATTTCTTATTAACATTTGAAGAAATCGATGTATGATGACAGGGCTGGGCAAGAA 1260
DB 1201 TTATTTCTTATTAACATTTGAAGAAATCGATGTATGATGACAGGGCTGGGCAAGAA 1260
QY 1261 CAGGGGCACTAGCTGCTTATTAAGTATTTAGTCCCTCGGTGTTGAGCTTAGCTTTG 1320
DB 1261 CAGGGGCACTAGCTGCTTATTAAGTATTTAGTCCCTCGGTGTTGAGCTTAGCTTTG 1320
QY 1321 ACCCTTCTTTTGAATCCAAATATACATTTAAACTGTGAATTCACATATCAATGCTATT 1380

Db 1321 ACCCTTCCTTTGATCCACAAATATCAATTAACCTGATTCACATCAATGATATT 1380
Qy 1381 TAAAGTCAATAGATTTTACCTATTAAGTGTGACCAAGTAAGTGTGTTGTTGTTG 1440
Db 1381 TAAAGTCAATAGATTTTACCTATTAAGTGTGACCAAGTAAGTGTGTTGTTGTTG 1440
Qy 1441 AAGTCCCCCAATGCGCCCAACTCGGATGTGGGGTACAGAGGTGAGGTGCACTATT 1500
Db 1441 AAGTCCCCCAATGCGCCCAACTCGGATGTGGGGTACAGAGGTGAGGTGCACTATT 1500
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Db 1501 AACAAATGTCATTAATATCTCATAGAGTACACTGCCAATAGATTTCAATGTTGCATG 1560
Qy 1561 TTGACCAAGAGGATTTTATATCTGAAGACATCACTATTAATACCTTGAGAGAG 1620
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Qy 1621 ATTTTGACCTGGCTTGAATAAAGTGTGCGAAGAAATGTATGAGCAATATATGAA 1680
Db 1621 ATTTTGACCTGGCTTGAATAAAGTGTGCGAAGAAATGTATGAGCAATATATGAA 1680
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Db 1681 ATAAACACACCTTTGTTAAAGATTAATAAAAAA 1712

RESULT 3
US-10-036-342-1
: Sequence 1, Application US/10036342
: Patent No. US20020090681A1
: GENERAL INFORMATION:
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Watanabe, Collin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhaog, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3030R1CS
: CURRENT APPLICATION NUMBER: US/10/036,342
: PRIOR FILING DATE: 2001-12-26
: PRIOR APPLICATION NUMBER: 60/085579
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/112514
: PRIOR FILING DATE: 1998-12-15
: PRIOR APPLICATION NUMBER: 60/113300
: PRIOR FILING DATE: 1998-12-22
: PRIOR APPLICATION NUMBER: 60/113430
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113605
: PRIOR FILING DATE: 1998-12-23
: PRIOR APPLICATION NUMBER: 60/113621
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: PRIOR APPLICATION NUMBER: 60/114140
: PRIOR FILING DATE: 1998-12-23
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: PRIOR FILING DATE: 1999-01-12
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: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/125774
: PRIOR FILING DATE: 1999-03-23
: PRIOR APPLICATION NUMBER: 60/125778
: PRIOR FILING DATE: 1999-03-23
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: PRIOR FILING DATE: 1999-03-24
: PRIOR APPLICATION NUMBER: 60/127035

: PRIOR FILING DATE: 1999-03-31
: PRIOR APPLICATION NUMBER: 60/127706
: PRIOR FILING DATE: 1999-04-05
: PRIOR APPLICATION NUMBER: 60/129122
: PRIOR FILING DATE: 1999-04-13
: PRIOR APPLICATION NUMBER: 60/130359
: PRIOR FILING DATE: 1999-04-21
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: PRIOR FILING DATE: 1999-05-25
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: PRIOR APPLICATION NUMBER: 09/644848
: PRIOR FILING DATE: 2000-08-22
: PRIOR APPLICATION NUMBER: 09/747259
: PRIOR FILING DATE: 2000-12-20
: PRIOR APPLICATION NUMBER: 09/816744
: PRIOR FILING DATE: 2001-03-22
: PRIOR APPLICATION NUMBER: 09/854208
: PRIOR FILING DATE: 2001-05-10
: PRIOR APPLICATION NUMBER: 09/854280
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: PRIOR FILING DATE: 2001-06-05
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: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: 09/908,827
: PRIOR FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: PCT/US99/10733
: PRIOR FILING DATE: 1999-05-14
: PRIOR APPLICATION NUMBER: PCT/US99/28551
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30720
: PRIOR FILING DATE: 1999-12-22
: PRIOR APPLICATION NUMBER: PCT/US00/05601
: PRIOR FILING DATE: 2000-03-01
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: 2000-05-22
: PRIOR APPLICATION NUMBER: PCT/US00/15264
: PRIOR FILING DATE: 2000-06-02
: PRIOR APPLICATION NUMBER: PCT/US00/23522
: PRIOR FILING DATE: 2000-08-23
: PRIOR APPLICATION NUMBER: PCT/US00/23328
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: 2000-12-01
: PRIOR APPLICATION NUMBER: PCT/US00/34956
: PRIOR FILING DATE: 2000-12-20
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: 2001-02-28

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; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 1
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-036-342-1

Query Match      100.0%; Score 1712; DB 12; Length 1712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGCATCTGCCGAGAGACCAAGCTCTGGAGCTGTGCTCTTCTCAGGGAGCTCTGA 60
Db      1  GGCATCTGCCGAGAGACCAAGCTCTGGAGCTGTGCTCTTCTCAGGGAGCTCTGA 60

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Db      61  GGCTCTGTGAGATCATGCTTTGGAGGACCTCATCTATTGGCACTGCTGGCTTTGTT 120

QY      121 TTTTCCTCCCTTTTGGCTGTGTCAAGATGATACATGAGTCTCTCACAACCCGAGACT 180
Db      121 TTTTCCTCCCTTTTGGCTGTGTCAAGATGATACATGAGTCTCTCACAACCCGAGACT 180

QY      181 ACCCCAGACTGAGTAAGTGTGTCAAGAGACTACAGCTTTGAGGCTTACCAAGGCC 240
Db      181 ACCCCAGACTGAGTAAGTGTGTGTCAAGAGACTACAGCTTTGAGGCTTACCAAGGCC 240

QY      241 CCCTGGGCCACCGGGCCCTCTGGCATTCAGGAACCATGGAACAATGGCAACATG 300
Db      241 CCCTGGGCCACCGGGCCCTCTGGCATTCAGGAACCATGGAACAATGGCAACATG 300

QY      301 AGGCACGTGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db      301 AGGCACGTGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360

QY      361 AGGGAAGCGGGGAGGATGGCCCAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 420
Db      361 AGGGAAGCGGGGAGGATGGCCCAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 420

QY      421 ACTTCAGATTGCATTCATGCTCTCTGGCAACCCACTTCAGCAATGAGAACAGTGGAT 480
Db      421 ACTTCAGATTGCATTCATGCTCTCTGGCAACCCACTTCAGCAATGAGAACAGTGGAT 480

QY      481 TATCTTCAGAGCTTATGAGACCAACATTTGGAATCTTTGATGTGATGATGATGAT 540
Db      481 TATCTTCAGAGCTTATGAGACCAACATTTGGAATCTTTGATGTGATGATGATGAT 540

QY      541 TGGGGCCCCAGTATCAGGTGTGATTTCTTCACCTTCAGCATGATGAGAGCATGAT 600
Db      541 TGGGGCCCCAGTATCAGGTGTGATTTCTTCACCTTCAGCATGATGAGAGCATGAT 600

QY      601 TGAAGAGTGTATGTGATCTTATGACAAATGCGCAACAGTCTTCAGCATGATGAG 660
Db      601 TGAAGAGTGTATGTGATCTTATGACAAATGCGCAACAGTCTTCAGCATGATGAG 660

QY      661 TGAATGAAGGGAATACATACATCCAGCAATCATGCTGTGAGAGCAAGCAAGG 720
Db      661 TGAATGAAGGGAATACATACATCCAGCAATCATGCTGTGAGAGCAAGCAAGG 720

QY      721 GGATGAGGTTGGCTGGCAATGGGCAATGGGCTCTCCATGGGAGCAACCAAGCTTCTC 780
Db      721 GGATGAGGTTGGCTGGCAATGGGCAATGGGCTCTCCATGGGAGCAACCAAGCTTCTC 780

QY      781 CACCTTTGACAGATCTCTGCTTTTGAACCTAAGTAATATATGATGAGTAAGCTCCAC 840
Db      781 CACCTTTGACAGATCTCTGCTTTTGAACCTAAGTAATATATGATGAGTAAGCTCCAC 840
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Db      781 CACCTTTGACAGATCTCTGCTTTTGAACCTAAGTAATATATGATGAGTAAGCTCCAC 840
QY      841 TTTGGGAGAGACTGTAGCTGAGCTGATTTGTAGATCTGAGCAACATTAAGTTGAGG 900
Db      841 TTTGGGAGAGACTGTAGCTGAGCTGATTTGTAGATCTGAGCAACATTAAGTTGAGG 900

QY      901 GTTTTACATTCCTGTATTCAAAATAATTAATGTTGCAATGTTGTTACAGCTACAGGTACA 960
Db      901 GTTTTACATTCCTGTATTCAAAATAATTAATGTTGCAATGTTGTTACAGCTACAGGTACA 960

QY      961 CCAATTAATGTTGAGCAATTCAGGGGCTCAGAGAAATCAACCAAAATATGCTTCTCAGA 1020
Db      961 CCAATTAATGTTGAGCAATTCAGGGGCTCAGAGAAATCAACCAAAATATGCTTCTCAGA 1020

QY      1021 TGACCTTGACATTAATATCTAGCAATCTTATACCTCTTCTGGCAGCTAAATATAT 1080
Db      1021 TGACCTTGACATTAATATCTAGCAATCTTATACCTCTTCTGGCAGCTAAATATAT 1080

QY      1081 TCTCCTTGAGGAGGAGTGAATATTTTTCATACAGAGATCATTTGCAAGAAAT 1140
Db      1081 TCTCCTTGAGGAGGAGTGAATATTTTTCATACAGAGATCATTTGCAAGAAAT 1140

QY      1141 TTGACTACTGCTTTTAAATTAATACAGTTTTCAGGAGCCCTGAAATTTTAAGTTCA 1200
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QY      1201 TTATCTTTTAAATATTTGAAGAAATGCGATGTAGTATATGACAGGGCTGGGGCAAGA 1260
Db      1201 TTATCTTTTAAATATTTGAAGAAATGCGATGTAGTATATGACAGGGCTGGGGCAAGA 1260

QY      1261 CAGGGGCACTAGTGCCTTTATAGCTAATTTAGTCCCTCCGCTGTTCAGCTTACCTTTG 1320
Db      1261 CAGGGGCACTAGTGCCTTTATAGCTAATTTAGTCCCTCCGCTGTTCAGCTTACCTTTG 1320

QY      1321 ACCCTTCTCTTTGATCCACAAATATCAATTAACCTGAAATTCACATACATGCTAAT 1380
Db      1321 ACCCTTCTCTTTGATCCACAAATATCAATTAACCTGAAATTCACATACATGCTAAT 1380

QY      1381 TAAAGTCAATGATTTTATAGCTATTAAGTGTGAGCAATATGAGTGTATTTTGTGT 1440
Db      1381 TAAAGTCAATGATTTTATAGCTATTAAGTGTGAGCAATATGAGTGTATTTTGTGT 1440

QY      1441 ATGTTCCCCCATGCGCCCAACTTCGATGTGGGAGTGGAGGTTGAGGTTGCTACTATT 1500
Db      1441 ATGTTCCCCCATGCGCCCAACTTCGATGTGGGAGTGGAGGTTGAGGTTGCTACTATT 1500

QY      1501 AACAAATGTCAATTAATCTCATAGAGGTACAGTCCCAATAGATATTCAAATGTTGCATG 1560
Db      1501 AACAAATGTCAATTAATCTCATAGAGGTACAGTCCCAATAGATATTCAAATGTTGCATG 1560

QY      1561 TTGACCAAGAGGATTTTATATCTGAAGACATACACTTTTAATTAATCTTAAAGGAAG 1620
Db      1561 TTGACCAAGAGGATTTTATATCTGAAGACATACACTTTTAATTAATCTTAAAGGAAG 1620

QY      1621 ATTGTAACCTGCTTTTGAATTAACCTGCGCAAGAAAATGTAATGAGCAATATATGGA 1680
Db      1621 ATTGTAACCTGCTTTTGAATTAACCTGCGCAAGAAAATGTAATGAGCAATATATGGA 1680

QY      1681 ATTAACACACCTTTGTTAAAGATAAAAAAA 1712
Db      1681 ATTAACACACCTTTGTTAAAGATAAAAAAA 1712

RESULT 4
US-09-822-849A-359
; Sequence 359, Application US/09822849A
; Patent No. US2002045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clair, Hilary
; APPLICANT: Reichel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
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: APPLICANT: Resnick, Richard J.
: APPLICANT: Gulukota, Kamalakara
: APPLICANT: Graham, James R.
: APPLICANT: Genetics Institute, Inc.
: TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
: FILE REFERENCE: GIN 6403
: CURRENT APPLICATION NUMBER: US/09/822, 849A
: CURRENT FILING DATE: 2001-09-04
: PRIOR APPLICATION NUMBER: 60/195, 582
: PRIOR FILING DATE: 2000-04-06
: NUMBER OF SEQ ID NOS: 598
: SOFTWARE: Patencin Ver. 2.0
: SEQ ID NO 359
: LENGTH: 1608
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-822-849A-359

Query Match      79.6%  Score 1363.2:  DB 10;  Length 1608;
Best Local Similarity 99.8%:  Pred. No. 0:
Matches 1365:  Conservative  0:  Mismatches  3:  Indels  0:  Gaps  0:

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QY  397 GGGCTACCCGGGGATTCACCAAGCACTCAGATTCATTCGCTTCCTGGCAACCA 456
DB  61 GGGCTACCCGGGGATTCACCAAGCACTCAGATTCATTCGCTTCCTGGCAACCA 120
QY  457 CTTCACCAATCAGAACAGAGGGGATTCCTTCACAGCTGTTGAGCAACACTTGAACCT 516
DB  121 CTTCACCAATCAGAACAGAGGGGATTCCTTCACAGCTGTTGAGCAACACTTGAACCT 180
QY  517 CTTTGATGTCAGTCTGTAGATTTGGGGCCCAAGTATCAGTGTGTATTTCTTCACCTT 576
DB  181 CTTTGATGTCAGTCTGTAGATTTGGGGCCCAAGTATCAGTGTGTATTTCTTCACCTT 240
QY  577 CAGCATGATGAAAGCATGAGATTTGAGAGAGTGTATGTACCTTATGCAATGGCA 636
DB  241 CAGCATGATGAAAGCATGAGATTTGAGAGAGTGTATGTACCTTATGCAATGGCA 300
QY  637 CACAGCTTCAGCATGTACAGTATGAATGAAGGGCAATCAGATACATCCAGCAATCA 696
DB  301 CACAGCTTCAGCATGTACAGTATGAATGAAGGGCAATCAGATACATCCAGCAATCA 360
QY  697 TCGTGTCTGTAAGCTAGCCAAAGGGGATGAGTTGGCTGCGAATGGCAATGGCGCTT 756
DB  361 TCGTGTCTGTAAGCTAGCCAAAGGGGATGAGTTGGCTGCGAATGGCGAATGGCGCTT 420
QY  757 CCATGGGAGACACCAACGCTTCTCCACCTTTGAGAGATTCCTCTTTTAAACTAGTA 816
DB  421 CCATGGGAGACACCAACGCTTCTCCACCTTTGAGAGATTCCTCTTTTAAACTAGTA 480
QY  817 AATATATGACTAGATAGCTCCACTTTGGGAGAGACTTGTAGCTGAGCTATTTGTTAG 876
DB  481 AATATATGACTAGATAGCTCCACTTTGGGAGAGACTTGTAGCTGAGCTATTTGTTAG 540
QY  877 ATCTGAGGAACATTTAAGTTGAGGGTTTACATTTGCTGTAATCAAAAATTAATGGTTGC 936
DB  541 ATCTGAGGAACATTTAAGTTGAGGGTTTACATTTGCTGTAATCAAAAATTAATGGTTGC 600
QY  937 AATGTGTTCACGCTACAGTACACCAATATTTGGACATTCAGGGGCTCGAAGAAAT 996
DB  601 AATGTGTTCACGCTACAGTACACCAATATTTGGACATTCAGGGGCTCGAAGAAAT 660
QY  997 CAACCAAAATATGCTCTGCATGACCTTGACTATATATACAGCATCTTATATCCTC 1056
DB  661 CAACCAAAATATGCTCTGCATGACCTTGACTATATATACAGCATCTTATATCCTC 720
QY  1057 TTTCCTTGGACCTAAAGATAATTCCTCTGACGAGGCTTGAATATTTTCTTAT 1116
DB  721 TTTCCTTGGACCTAAAGATAATTCCTCTGACGAGGCTTGAATATTTTCTTAT 780

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QY  1117 CACAGAGTCATTTGCAAGAAATTTGACTACTGCTGTTTAAATTAATACAGATTTCA 1176
DB  781 CACAGAGTCATTTGCAAGAAATTTGACTACTGCTGCTGTTTAAATTAATACAGATTTCA 840
QY  1177 GGAACCCCTGAAGTTTAAATTCATTTCTTTATACATTTGAGAGAAATCGATAGT 1236
DB  841 GGAACCCCTGAAGTTTAAATTCATTTCTTTATACATTTGAGAGAAATCGATAGT 900
QY  1237 GATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCTTATTTAGTATTTAGTGC 1286
DB  901 GATATGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCTTATTTAGTATTTAGTGC 960
QY  1297 CCTCCGTTACCTAGCTTACGCTTTGACCCCTTCTCTTTGATCCACAAATACATTAACCT 1356
DB  961 CCTCCGTTACCTAGCTTACGCTTTGACCCCTTCTCTTTGATCCACAAATACATTAACCT 1020
QY  1357 CTGAATTCACATTCATTCATTTTAAAGTCAATAGATTTTAAAGTCTTAAAGTCTGAC 1416
DB  1021 CTGAATTCACATTCATTCATTTTAAAGTCAATAGATTTTAAAGTCTTAAAGTCTGAC 1080
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QY  1477 GTGAGAGGTTGAGCTTACATTTAACAATGTATTAATATCTCATAGAGGTACAGTGC 1536
DB  1141 GTGAGAGGTTGAGCTTACATTTAACAATGTATTAATATCTCATAGAGGTACAGTGC 1200
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DB  1201 CAATGATATTCATTAATCTTCATGTTGACCAAGAGGATTTTATATCTGAAGAACATACAC 1260
QY  1597 TATTAATTAATACCTTAGAAGAAAGATTTTACCTGCTTATGATTAAGAACTGGCAAGAA 1656
DB  1261 TATTAATTAATACCTTAGAAGAAAGATTTTACCTGCTTATGATTAAGAACTGGCAAGAA 1320
QY  1657 AATATGATGAGCAATATATGAAATTAACACACCTTTGTTAAGATA 1704
DB  1321 AATATGATGAGCAATATATGAAATTAACACACCTTTGTTAAGATA 1368

RESULT 5
US-09-864-761-12152
: Sequence 12152, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
: FILE REFERENCE: Aeomica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669

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RESULT 10

US-09-738-973-151

Sequence 151, Application US/09738973

Patent No. US20020110563A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
 APPLICANT: Henderson, Robert A.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Filing, Steven P.
 APPLICANT: Mohamach, Radodoh
 APPLICANT: Algate, Paul A.
 APPLICANT: Secrist, Heather
 APPLICANT: Indrias, Carol Joseph
 APPLICANT: Benson, Darin R.
 APPLICANT: Elliott, Mark
 APPLICANT: Mannion, Jane
 APPLICANT: Kalos, Michael D.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121.475C9
 CURRENT APPLICATION NUMBER: US/09/738,973
 CURRENT FILING DATE: 2000-12-14
 NUMBER OF SEQ ID NOS: 587
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 151
 LENGTH: 3275
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-738-973-151

Query Match 4.6%; Score 78.8; DB 10; Length 3275;
 Best Local Similarity 52.4%; Pred. No. 1.4e-11;
 Matches 173; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 479 ATTATCTCAGCAGTGTGACACCAATTTGGAACCTTTGANGTCATGACTGAGTACA 538
 DB 2445 ATTTGGTTGATCTTCTCTGTAACACTTGAAGAACTTTGATCTTACGCTGTAGA 2504
 QY 539 TTTGGGCCCCAGTATGAGTGTATTTCTTACCTTCAGCATGATGAAGCATGAGAT 598
 DB 2505 TTTATTTGCCAGTAATGAGCATTTACGTTTTCATTTTACATCTTAAGCTGGCAGTG 2564
 QY 559 GTTGAAGAGTATGTTGATGCTTATGCAACAATGGCAACAGCTTTCAGCATGTACAGC 658
 DB 2565 AATGTGCCACGTATGTACCTCATGAAGATGAAGAGTGTGATACACCTATGCGC 2624
 QY 659 TATGAATGAAGGCAATCATCATCCAGCATTCATGCTGCTGTAGAGTACGCCAA 718
 DB 2625 AATGATGCTCTCCAGACCAATGAACCTGTACCAATTCATGCAATTCCTTCCAG 2684
 QY 719 GGGGATGAGTTTGGCTGCGAATGGGAGGCTCTCCATGGGAGACCAACGCTTC 778
 DB 2685 GGAGACCGAATATGTTAGCTGTGACAGGGGAGCAATTTATGAAGTGTGGAATAT 2744
 QY 779 TCCACCTTTGCAAGATTCTCTCTTTGAA 808
 DB 2745 TCTAGTTTTCAGGCTATCTTCTTATCAA 2774

RESULT 11

US-09-776-976-5

Sequence 5, Application US/09776976

Patent No. US20020037849A1

GENERAL INFORMATION:

APPLICANT: Fruebis, Joachim
 APPLICANT: Erickson, Mary Ruth
 APPLICANT: Yen, Frances
 APPLICANT: Bihain, Bernard
 TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
 FILE REFERENCE: 76.US4.REG
 CURRENT APPLICATION NUMBER: US/09/776,976
 CURRENT FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: US 09/758,055

PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: US 60/176,228
 PRIOR FILING DATE: 2000-01-14
 PRIOR APPLICATION NUMBER: US 60/198,087
 PRIOR FILING DATE: 2000-04-13
 PRIOR APPLICATION NUMBER: US 60/299,881
 PRIOR FILING DATE: 2000-09-01
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patent.pm
 SEQ ID NO 5
 LENGTH: 4517
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-776-976-5

Query Match 4.4%; Score 74.6; DB 10; Length 4517;
 Best Local Similarity 50.4%; Pred. No. 2.5e-10;
 Matches 210; Conservative 0; Mismatches 204; Indels 3; Gaps 1;

QY 219 GCTTTCAGAGCTACCAAGGCCCTTGGGCCACCGGCCCTCTGCGATTCCAGGAAC 278
 DB 151 GCATCCAGGGCATCCGGCCATTAATGGGCCCCAGGCCGTGATGCGAGATGGACCC 210
 QY 279 ATGAAGCAATGCAACAATGAGGCCACTGTATGATGAAGAGCAAGGTGAGAAGGCC 338
 DB 211 CTGTGAGAGGGTGAAGAAGAGATCCAGATGCTTATTTGCTCTAAGGAGACATCGTG 270
 QY 339 ACAAGGTGACCTGGGCGCTCGAGGGGAGCGGGGCGACCATGCCCCAAGGAGAGAG 398
 DB 271 AAACCGGAGTACCCCGGCGCTGAAGGTCCCGAGGCTTCCGGAGATCCACGACAGAA 330
 QY 399 GCTACCGGGG--GATTCACACCACTTCAGATTCATGCTTCTGCGCAACC 455
 DB 331 GAGAACCTGGAGAGAGTCTTATGTATACCGCTCAGCATTCAGTGTGGAGTGGAGACT 390
 QY 456 ACTTCAGCAATCAGACAGTGGATTTATCTTCAGCAGAGTGTGAGACCAATTTGGAAT 515
 DB 391 ACGTTACTATCCCAACATGCGCATTCGCTTTACCAAGATCTTACAAATCAGCAAAAC 450
 QY 516 TCTTGAATGTCATGACTGTGATGTTGGGCCCGCAGTATCAGGTGTGATTTCTTACCT 575
 DB 451 ACTATGATGGCTCCACTGTAAATTCACATGACATTCCTGGGCTGTACTACTTGGCT 510
 QY 576 TCAGCATGATGAGCATGAGATGTTGAGGAAGTATGATGATCTTATGCAAGATG 632
 DB 511 ACCACATCAGATCTATATGAAGATGTGAAGTACGCTCTTCAAGAGACAAAG 567

RESULT 12

US-09-758-055-5

Sequence 5, Application US/09758055

Patent No. US20020058617A1

GENERAL INFORMATION:

APPLICANT: Fruebis, Joachim
 APPLICANT: Erickson, Mary Ruth
 APPLICANT: Yen, Frances
 APPLICANT: Bihain, Bernard
 TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
 FILE REFERENCE: 76.US4.REG
 CURRENT APPLICATION NUMBER: US/09/758,055
 CURRENT FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: US 60/176,228
 PRIOR FILING DATE: 2000-01-14
 PRIOR APPLICATION NUMBER: US 60/198,087
 PRIOR FILING DATE: 2000-04-13
 PRIOR APPLICATION NUMBER: US 60/299,881
 PRIOR FILING DATE: 2000-09-01
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patent.pm
 SEQ ID NO 5
 LENGTH: 4517
 TYPE: DNA
 ORGANISM: Homo sapiens

RESULT 2
AX039945 1696 bp DNA linear PAT 18-NOV-2000
LOCUS
DEFINITION Sequence 1 from Patent W00063377.
ACCESSION AX039945
VERSION AX039945.1 GI:11229969
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Piddington, C.S. and Bishop, P.D.
TITLE Adipocyte complement related protein homolog zacr3
JOURNAL Patent: WO 0063377-A 1 26-OCT-2000;
ZymoGenetics, Inc. (US)
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/translation="MLWRQLIYWQLLALFLFPLCLCODEYMEPSQTGGLPDDSKCH
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BASE COUNT 482 a 355 c 386 g 473 t
ORIGIN
Query Match 99.1%; Score 1696; DB 6; Length 1696;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1696: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

481 GCAGTGTGAGACCAACATTGGAACCTCTTGATGTCATGATGGTAGATTGGGGCCC 540
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QY 669 AGGCAATCAGATACATCAGCAATCAGCAATCAGCAATCAGCAATCAGCAATCAG 728
DB 661 AGGCAATCAGATACATCAGCAATCAGCAATCAGCAATCAGCAATCAGCAATCAG 720
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DB 721 TTTGGCTGCGAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 780
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DB 781 CAGGATTCCTGCTTTGAACTAGTAATATATGATGATGATGATGATGATGATGAT 840
QY 849 AGACTGTAGCTGAGCTGATTTGTACGATCTGAGCAATTAAGTTGAGGCTTTTACA 908
DB 841 AGACTGTAGCTGAGCTGATTTGTACGATCTGAGCAATTAAGTTGAGGCTTTTACA 900
QY 909 TTGCTGTATTCAGAAATTAATTTGCTGCAATGTTTACGCTGACAGTACCAATTA 968
DB 901 TTGCTGTATTCAGAAATTAATTTGCTGCAATGTTTACGCTGACAGTACCAATTA 960
QY 969 GTTGACAAATTCAGGGGCTGAGAAATCAACCAAAATGCTTCAGATGAGCTTG 1028
DB 961 GTTGACAAATTCAGGGGCTGAGAAATCAACCAAAATGCTTCAGATGAGCTTG 1020
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DB 1021 ACTAATATACAGCAATCTTATACCTCTTCCCTGGCACTTAAAGTATATCTCTCT 1080
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DB 1561 AGGATTTTATTCATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1620

QY 1629 CTGGCTTTAGATAAACTGTGGCAGAAAAATGTATGACATATATGAAATAAACAC 1688
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DB 1621 CTGGCTTTAGATAAACTGTGGCAGAAAAATGTATGACATATATGAAATAAACAC 1680
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QY 1689 ACCCTTTGTTAAAGATA 1704
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DB 1681 ACCCTTTGTTAAAGATA 1696
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RESULT 3
AF329837 1710 bp mRNA linear PRI 12-MAR-2001
AF329837
LOCUS Homo sapiens complement-clq tumor necrosis factor-related protein
DEFINITION (CPRP3) mRNA, complete cds.
ACCESSION AF329837
VERSION AF329837.1 GI:13274519
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1710)
AUTHORS Piddington, C.S. and Bishop, P.
TITLE Homo sapiens complement-clq tumor necrosis factor-related protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1710)
AUTHORS Piddington, C.S. and Bishop, P.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Ave. East, Seattle, WA 98102, USA
FEATURES
source 1. 1710
/organism="Homo sapiens"
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BASE COUNT 484 a 358 c 392 g 476 t
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Query Match 99.1%; Score 1696; DB 9; Length 1710;
Best local similarity 100.0%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GCCCGAGAGACACACGCTCTGTGAGCTCTGTCTTTCTAGGAGACTCTGAGGCTCTG 67
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DB 75 TTGAGATCATGTCTTGGAGGACCTCATATGSCAACGCTGGCTTTGTTTCTC 134
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QY 128 CCTTTTGCCTGTGTCAAGATGATATACATGAGACTCTCCACAAACCGAGAGACTACCCCA 187
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DB 135 CTTTTCCTGTGTCAAGATGATATACATGAGACTCTCCACAAACCGAGAGACTACCCCA 194
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QY 188 GACTGCAGTAAGTGTGTATGAGACTACAGCTTTTGAGGCTACCAAGGCCCTCCCTGGG 247
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DB 195 GACTGCAGTAAGTGTGTATGAGACTACAGCTTTTGAGGCTACCAAGGCCCTCCCTGGG 254
QY 248 CCACCGGGCCCTCTGTGACATTCAGAGAAACCATGAAACATATGAGACCTACT 307
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DB 255 CCACCGGGCCCTCTGTGACATTCAGAGAAACCATGAAACATATGAGACCTACT 314
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QY 308 GGTTCATGAGAGAGCCAAAGGTGAGAAAGGCGACAAAGGTACCTGGGGCTCCGAGGGAG 367
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DB 1275 ACTAGCTGCTTATTAATGATATTTAGTCCCTCCGCTGTTACGCTTGAACCTTTT 1334
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QY	1338	CTTTTGATCCACAAATATCATTTAAACTGTGAACTTCACATACATGCTATTTTAAAGTC	1387
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QY	1388	AATAGATTTTGGCTTTAAAGTCCTTGACACAGTAATGCTGTTATTTTGGTATGTTCC	1447
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QY	1448	CCACATATGCCCCCAACTTCGGATGTGGGGGTCCAGAGGTTGAGGTTCACTATTAACAAT	1507
Db	1455	CCACATATGCCCCCAACTTCGGATGTGGGGGTCCAGAGGTTGAGGTTCACTATTAACAAT	1514
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Db	1515	GTCAATAATATCTCATAGAGGTACAGTCCCAATATATTTCAAAATGTTGATGACCA	1574
QY	1568	GAGGATTTTATATCTGAAGAATACATACACTATTAAATACCTTAGAGAAAGATTTTGA	1627
Db	1575	GAGGATTTTATATCTGAAGAATACATACACTATTAAATACCTTAGAGAAAGATTTTGA	1634
QY	1628	CCTGCTTTAGATTAATACTGTGCGAAGAAAATGTAATAGCAATATATGGAATAAACA	1687
Db	1635	CCTGCTTTAGATTAATACTGTGCGAAGAAAATGTAATAGCAATATATGGAATAAACA	1694
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Db	1695	CACCTTTGCTTAAGAT 1710	
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AX136339			
LOCUS	AX136339	1709 bp	DNA
DEFINITION	Sequence 261 from Patent EP1067182.		linear
ACCESSION	AX136339		
VERSION	AX136339.1	GI:14272745	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1709) Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K. Secretory protein of membrane protein Patent: EP 1067182-A 261 10-JUN-2001; Helix Research Institute (JP) Location/Qualifiers 1..1709 /organism="Homo sapiens" /db_xref="taxon:9606" 89..829 /note="unnamed protein product" /codon_start=1 /protein_id="CAC39811.1" /db_xref="GI:14272746" /translation="MIMROLIYMOILAIFPLPCLODEVWESPOTGGLPDPCKSCCH CDYSRGTQCPGPPGPPGPIGNNMNNKATGHBKKGKGRKDGLEPGEGRGQRH PKGEKGTGPIPELQIAFMASLATFHSNÖNGILFSSVETIIGNFDMTGRFAPVYS GVYFETFSMKHEDEVYVYVILMHNGNTVFEMYSYEMKGRDTSNNHAYVLKLARGDEV WLRMNGALHMDHDFRSTFAGFLFETG"		
FEATURES	source		
CDS			
BASE COUNT	480 a	363 c	390 g
ORIGIN			
Query Match	99.0%;	Score 1695.4;	DB 6; Length 1709;
Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 1696;	Conservative	0; Mismatches	1; Indels
		Gaps	0;
QY	1	GGCATCTGCCGAGGAGACACAGCTCCTTGACAGCTCGCTCTTCCAGAGGAGACTGGA	60
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QY	61	GGCTCTGTTGAGAAATCATCTTTGAGAGGAGCTCATCTATTGGCAACTGCTGGCTTTGT	120

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Q	y	121	TTTTCTCCCTTTTGGCTGTGTCAAGATGAAATACATGAGATGCTTCACAAACGGAGACT	180
D	b	133	TTTCCTCCCTTTTGGCTGTGTCAAGATGAAATACATGAGATGCTTCACAAACGGAGACT	192
Q	y	181	ACCCCAAGCTGACGTAAGTGTGTATGAGACACTACAGCTTTGAGAGCTACCAAGGCC	240
D	b	193	ACCCCAAGCTGACGTAAGTGTGTATGAGACACTACAGCTTTGAGAGCTACCAAGGCC	252
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D	b	253	CCCTGGGACCGGGGCCCTCTGGCAATTCAGGAACCATGAAACAAATGGCAACATGG	312
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D	b	313	ACCCATGCTCATGAAAGGAGCCAAAGGTGAGAAAGGCGCAAAAGGTGACCTGGGGCTCG	372
Q	y	361	AGGGGAGCGGGGGCGACCATGCGCCCAAGAGAGAGAAAGGCTACCCGGGGATTCCACAGA	420
D	b	373	AGGGGAGCGGGGGCGACCATGCGCCCAAGAGAGAGAAAGGCTACCCGGGGATTCCACAGA	432
Q	y	421	ACTTCAGATTCGATTCATGAGCTTCTCTGGCAACCCACTTCAGCAATGAGAAAGTGGAT	480
D	b	433	ACTTCAGATTCGATTCATGAGCTTCTCTGGCAACCCACTTCAGCAATGAGAAAGTGGAT	492
Q	y	481	TATCTTCACAGCTGTGAGACCAACATTTGGAACCTTTTGATGTCTATGATCTGTAGATT	540
D	b	493	TATCTTCACAGCTGTGAGACCAACATTTGGAACCTTTTGATGTCTATGATCTGTAGATT	552
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D	b	553	TGGGGGCCAGTATACAGGTGTGTATTCTTCACCTTCAGCATGATGAGCATGAGATGT	612
Q	y	601	TGAGGAAGTGTATGTACTTATGACAAATGGCAACAGTCTTCAGCATGTACACTA	660
D	b	613	TGAGGAAGTGTATGTACTTATGACAAATGGCAACAGTCTTCAGCATGTACACTA	672
Q	y	661	TGAATGGAAGGCAATACATACATTCACACATCATGCTGTCTGAAGCTAGCCAAAG	720
D	b	673	TGAATGGAAGGCAATACATACATTCACACATCATGCTGTCTGAAGCTAGCCAAAG	732
Q	y	721	GGATGAGTTTGGCTCGAATGGGCAATGGCGCTCTCCATGGGGACCAACAGCTTCTC	780
D	b	733	GGATGAGTTTGGCTCGAATGGGCAATGGCGCTCTCCATGGGGACCAACAGCTTCTC	792
Q	y	781	CACCTTTGACAGATTTCTCTCTTTTGAACATAAGTAATATATGACTAGAAATACCTCAC	840
D	b	793	CACCTTTGACAGATTTCTCTCTTTTGAACATAAGTAATATATGACTAGAAATACCTCAC	852
Q	y	841	TTTTGGGAAGACTTGTAGCTGAGCTGATTTGTAACGATCTGAGGAACATTTAAATTTAGG	900
D	b	853	TTTTGGGAAGACTTGTAGCTGAGCTGATTTGTAACGATCTGAGGAACATTTAAATTTAGG	912
Q	y	901	GTTTTACATTTGCTATTTCAAAAATTTATTTGGTGAATGTTTGTACGCTACAGGTACA	960
D	b	913	GTTTTACATTTGCTATTTCAAAAATTTATTTGGTGAATGTTTGTACGCTACAGGTACA	972
Q	y	961	CCATATATGTTGACAAATTTAGGGGCTCAGAGAAATTAACCAAAATATGCTTCTCAGA	1020
D	b	973	CCATATATGTTGACAAATTTAGGGGCTCAGAGAAATTAACCAAAATATGCTTCTCAGA	1032
Q	y	1021	TGACCTTGACTATATACAGACATCTTTCACATCTTTCTGGACCTTAAAGATTAAT	1080
D	b	1033	TGACCTTGACTATATACAGACATCTTTCACATCTTTCTGGACCTTAAAGATTAAT	1092
Q	y	1081	TCCTCTCTGACGAGTTTGAATATTTTTTTCTATCACAAGAACTCATTTTGCAAAAGATT	1140
D	b	1093	TCCTCTCTGACGAGTTTGAATATTTTTTTCTATCACAAGAACTCATTTTGCAAAAGATT	1152
Q	y	1141	TTGACTACTCTGCTTTTAAATTTAATACAGTTTTCAGGAACCCCTGAAGTTTAAAGTTCA	1200

Db	1153	TTGACTACCTCTCTTTAAATTAAATACAGTTTTACGAAACCCCGAACTTTTAAGTTCA	1212
OY	1201	TTATTCCTTTATACATTTAGAGAAATCGGATGTAGTATATGACAGGCTGGGGCAAGAA	1260
Db	1213	TTATTCCTTTATACATTTGAGAGAAATCGGATGTAGTATATGACAGGCTGGGGCAAGAA	1272
OY	1261	CAGGGGCACTACTGCTGCTTATAGCTAAATTTAGTGGCCGCTGTTCACTTAAGCTTTG	1320
Db	1273	CAGGGGCACTACTGCTGCTTATAGCTAAATTTAGTGGCCGCTGTTCACTTAAGCTTTG	1332
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Db	1573	TTGACCAGAGGGATTTTATATCTGGAAGAACATACACTATTATTAATACCTTAGAGAAAG	1632
OY	1621	ATTTCGACCTGGCTTTAGATTAATAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA	1680
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LOCUS	AX191537	1927 bp	DNA
DEFINITION	Sequence 59 from Patent WO0149728.		linear
ACCESSION	AX191537		
VERSION	AX191537.1	GI:15209727	
KEYWORDS			
SOURCE	human.		

REFERENCE
Euharziota, Euthetia; Chordata; Crinacea; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
1 (bases 1 to 1927)
AUTHORS
Kato, S. and Kimura, T.
TITLE
Human proteins having hydrophobic domains and dnas encoding these
proteins: WO 0149728-A-59 12-JUL-2001.
JOURNAL
Patent: Ino. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
FEEDBACK

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CDS    89. .760
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Query Match	89.2%	Score 1527	DB 6	Length 1927
Best Local Similarity	99.9%	Prod. No. 0		
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Db	390	AGCTTCACAAACCGGAGACTACCCCAAGACTGCAAGTAAGTGTGATGGAGACTACA	449	
Oy	219	GCTTTTCGAGGCTACCAAGGCCCCCTGGGCCCCCGGCGCTCTTGCAATTCACGAAACC	278	
Db	450	GCTTTTCGAGGCTACCAAGGCCCCCTGGGCCCCCGGCGCTCTTGCAATTCACGAAACC	509	
Oy	279	ATGGAACAATGGCAACAATGAGGCACTGGTCATGAAAGGACCAAGGTGAAAGGCG	338	
Db	510	ATGGAACAATGGCAACAATGAGGCACTGGTCATGAAAGGACCAAGGTGAAAGGCG	569	
Oy	339	ACAAAGGTACCTGGGGGCTTCGAGGGGAGCGGGGACAGATGGCCCCCAAGAGGAAG	398	
Db	570	ACAAAGGTACCTGGGGGCTTCGAGGGGAGCGGGGACAGATGGCCCCCAAGAGGAAG	629	
Oy	399	GCTACCCGGGATTCACACCACTTCAGATTGCAATTCATGGCTCTCTGGCAACCCACT	458	
Db	630	GCTACCCGGGATTCACACCACTTCAGATTGCAATTCATGGCTCTCTGGCAACCCACT	689	
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Db	690	TCAGCAATCAGACAGTGGGATTAATCTTCAGCAGTGTGACACCAACTTGGAAACTTCT	748	
Oy	519	TTGATGTACATGCTGTGTGATTTGGGGCCCCAGATACAGTGTGATTTCTTCACCTTCA	578	
Db	749	TTGATGTACATGCTGTGTGATTTGGGGCCCCAGATACAGTGTGATTTCTTCACCTTCA	808	
Oy	579	GCATATGAGAGCATGAGGATGTTGAGAAAGTATGTGTACTTATGCACATGGCAACA	638	
Db	809	GCATATGAGAGCATGAGGATGTTGAGAAAGTATGTGTACTTATGCACATGGCAACA	868	
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Db	1169	TGTTTTCACGCTACAGGTACACCAATATATTGGACATTCACAGGGGCTCGAAGAAATCA	1228	
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Db	1349	CAGAAGCATTTTGCAGAAATTTTGACACTCTCTTATTTATTAATACAGTTTACG	1408	
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QY 1599 TTAATTAATACCTTAGAAGAAAGATTTTGACCTGCTTTAGATTAATACTGTGCCAGAAA 1658
Db 1829 TTAATTAATACCTTAGAAGAAAGATTTTGACCTGCTTTAGATTAATACTGTGCCAGAAA 1888
QY 1659 ATGTAAATGAGCATATATGGAATTAACAACACCTTTGTT 1697
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RESULT 6
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LOCUS BC016021
DEFINITION Homo sapiens, Similar to complement-clq tumor necrosis factor-related protein; likely ortholog of mouse COR526 (collagenous repeat-containing sequence of 26-kDa protein), clone MGC:27511 IMAGE:4720611, mRNA, complete cds.
ACCESSION BC016021
VERSION BC016021.1 GI:16359108
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1426)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA.
REMARK NIH-MGC project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
Series: IRAL Plate: 38 Row: P Column: 18.
Location/Qualifiers

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Best Local Similarity 99.5%; Pred. No. 2.9e-313;
Matches 1284; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 482 ATCTTCAGACGTGTGAGACCAACATGGAACCTCTTGTATGTCATGCTGTAGATTT 541
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DEFINITION		2 Ordered pieces.	
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VERSION		AC026707.5 GI:19224781	
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ORGANISM		Homo sapiens.	
REFERENCE		Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 155013)	
TITLE		DOE Joint Genome Institute.	
AUTHORS		Sequencing of Human Chromosome 5	
REFERENCE		Unpublished	
JOURNAL		2 (bases 1 to 155013)	
TITLE		DOE Joint Genome Institute.	
AUTHORS		Direct Submission	
REFERENCE		Submitted (23-MAR-2000) Production Sequencing Facility, DOE Joint	
JOURNAL		Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	
TITLE		3 (bases 1 to 155013)	
AUTHORS		DOE Joint Genome Institute.	
REFERENCE		Direct Submission	
JOURNAL		Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint	
TITLE		Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	
AUTHORS		On Mar 7, 2002 this sequence version replaced gi:19256664.	
COMMENT		-----Genome Center	
		Center: Joint Genome Institute	
		Center Code: JGI	
		Web site: http://www.jgi.doe.gov	

	Project information	
	Center Project Name: 656404	
	Center clone name: CTRB_HL_2075C7	

	Summary Statistics	
	Consensus quality: 153352 bases at least Q40	
	Consensus quality: 154674 bases at least Q30	
	Consensus quality: 154871 bases at least Q20	
	Estimated insert size: 171000; pulse field gel estimation	
	Estimated insert size: 154913; sum-of-contigs estimation	
	Quality coverage: 9.64 in Q20 bases; pulse field gel estimation	
	Quality coverage: 10.64 in Q20 bases; sum-of-contigs estimation.	
	* NOTE: This is a "working draft" sequence. It currently	
	* consists of 2 contigs. Gaps between the contigs	
	* are represented as runs of N. The order of the pieces	
	* is believed to be correct as given, however the sizes	
	* of the gaps between them are based on estimates that have	
	* provided by the submittor.	
	* This sequence will be replaced	
	* by the finished sequence as soon as it is available and	
	* the accession number will be preserved.	
	*	
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Qy 1671 ATATATGGAATTAACACACCTTTGTTAAGATA 1704
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RESULT 8
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LOCUS Homo sapiens chromosome 5 clone CTD-2340N2, complete sequence.
AC008954
AC008954.6 GI:14329063
VERSION HMG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Direct Submission
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 90111)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (27-APR-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 90111)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Jun 8, 2001 this sequence version replaced gi:13911891.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.1.
STS Content:
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WI-856 G02835
SHGC-36018 G30037.
Location/Qualifiers
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/clone="CTD-2340N2"
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Best Local Similarity 99.5%; Pred. No. 8e-254;
Matches 1049; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 651 TGTACAGTATGAATGAAGGAGGCAATCAGATACATCAGCAATCAGTGTGCTGAAGC 710
Db 10367 TTTCCAGCTATGAATGAAGGAGGCAATCAGATACATCAGCAATCAGTGTGCTGAAGC 10426
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Db 11207 GTTCACATATAACAATGTCTATTAATATCTCATAGAGTACAGTGGCAATAGATATTCAA 11266
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RESULT 9
AX136588 810 bp DNA linear PAT 30-MAY-2001
LOCUS Sequence 510 from Patent EP1067182.
DEFINITION AX136588
ACCESSION AX136588
VERSION AX136588.1 GI:14272992
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 810)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 510 10-JAN-2001;
Helix Research Institute (JP)
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Best Local Similarity 98.9%; Pred. No. 3.4e-183;
Matches 791; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

OY 1 GGCATCTGCGCCGAGAGACACACGCTCTGAGCTCTGCTGCTCTCAGAGAGACTCTGA 60
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OY 61 GGCCTGTGTGAGAAATCATGCTTTGGAGCGAGCTCATATTGCGCAACTGCTGGCTTTGTT 120
Db 73 GGCCTGTGTGAGAAATCATGCTTTGGAGCGAGCTCATATTGCGCAACTGCTGGCTTTGTT 132
OY 121 TTTCTCTCCCTTTTCCCTGCTGTGCAAGATGAATACATGAGTGTCCACAAACCGAGAGACT 180
Db 133 TTTCTCTCCCTTTTCCCTGCTGTGCAAGATGAATACATGAGTGTCCACAAACCGAGAGACT 192
OY 181 ACCCCAGACACTGCAATAGTGTGTTCATGAGACTACAGCTTTGAGAGCTTACCAAGGCC 240
Db 193 ACCCCAGACACTGCAATAGTGTGTTCATGAGACTACAGCTTTGAGAGCTTACCAAGGCC 252
OY 241 CCTTGGGCGACCGGCGCTCTGCGCATTCAGAGAACCATGGAACATGCGCAACATG 300
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OY 301 AGCCACTGCTGTGAAGAGCCAAAGGTGAGAGGGCGCAAAAGTGTGACCTGGGCGCTCG 360
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OY 361 AGGGAAGCGGGGCGAGCATGGCCCCAAGAGAGAGAGGCGTACCGGGGATTCCACCGA 420
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OY 481 TATCTTCACACTGTGTTGAGACCAACATTGGAACCTTTGATGTCATACAGTGTAGATT 540
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Db 673 TGAATGAAGGCGCAATCAGATACATCCAGCAATCATGCTGTGCTGAA-CTAGCCCAAAG 731
OY 721 GGATGAGGTTTGGCTGCGCAATGSGCAATGGCGCTCTCCATGGGGAGCCACCAAGCTTTC 780
Db 732 GGATGAGGTTTGGCTGCGCAATGSGCAATGGCGCTCTCCATGGGGAGCCACCAAGCTTTC 790
OY 781 CACTTTCGAGGATTCCTGC 800
Db 791 CACTTTCGAGGATTCCTGC 810

RESULT 10
AX039955 1117 bp DNA linear PAT 18-NOV-2000
LOCUS Sequence 11 from Patent WO0063377.
DEFINITION AX039955
ACCESSION AX039955
VERSION AX039955.1 GI:11229976
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 1117)
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte complement related protein homolog zacrp3
JOURNAL Patent: WO 0063377-A 11 26-OCT-2000;
ZymoGenetics, Inc. (US)
FEATURES
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Best Local Similarity 85.5%; Pred. No. 3e-165;
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Db 106 GAGCCATGCTCTGGAGAGCGACGACATCTGTGACACTCTGCTTGTGCTTTCCCTCCAT 165
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QY	492	GTTTGTGAGACCAACATTGGAAACTCTTTGATGTGCATGATGCTGTAGATTGGGGCCCCAG	551
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QY	911	GCTGTATTCAAAAAATTAATTTGTTGTCGAATGTTGTTCCAGCCTCAGGTACCAATTAATCT	970
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QY	971	TGGACAATTCAGGGGCTCA 989	
Db	1006	TGGATGCTTCAGGGGCTCA 1024	

REFERENCE	1 (bases 1 to 1879)			
AUTHORS	Maeda,T., Abe,M., Kurisu,K., Jikko,A. and Furukawa,S.			
TITLE	Molecular Cloning and characterization of a novel gene, CONS26, encoding a putative secretory protein and its possible involvement in skeletal development			
JOURNAL	J. Biol. Chem. 276 (5), 3628-3634 (2001)			
MEDLINE	21264842			
PUBMED	11071891			
REFERENCE	2 (bases 1 to 1879)			
AUTHORS	Maeda,T. and Jikko,A.			
TITLE	Direct Submission			
JOURNAL	Submitted (18-MAR-2000) Radiology and Radiation Oncology, Osaka University School of Dentistry, 1-8 Yamadaoka, Suita, Osaka 565-0871, Japan			
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Db 3 GTT 1
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AX191527 672 bp DNA linear PAT 15-AUG-2001
LOCUS AX191527
DEFINITION Sequence 49 from Patent WO0149728.
ACCESSION AX191527
VERSION AX191527.1 GI:15209709
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 672)
AUTHORS Kato,S. and Kimura,T.
TITLE Human proteins having hydrophobic domains and dnas encoding these
proteins
JOURNAL Patent: WO 0149728-A 49 12-JUL-2001;
Proteome Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
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Db 482 ACAAGGTGACTGGGGCTTCGAGGGAGACGGGGGACAGATGGCCCAAGAGAGAGAGG 541
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AX079496 546 bp DNA linear PAT 22-FEB-2001
LOCUS AX079496
DEFINITION Sequence 240 from Patent WO0107611.
ACCESSION AX079496
VERSION AX079496.1 GI:13159056
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 546)
AUTHORS Baker,K.P., Goddard,A. and Wood,W.I.
TITLE Human polypeptides and methods for the use thereof
JOURNAL Patent: WO 0107611-A 240 01-FEB-2001;
Genentech, Inc. (US)
FEATURES
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Search completed: January 15, 2003, 18:56:35
Job time : 4496 secs

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Title: US-10-036-041-1

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	751.8	43.9	776	12	BG186424 RST5388 A
2	743.4	43.4	874	12	BG186928 RST5905 A
3	704.4	41.1	1103	14	BM924169 AGENCOURT
4	692.6	40.5	762	12	BG201468 RST20685
5	685.2	40.0	828	12	BG400260 60246452
6	673.8	39.4	815	13	BT57458 603029396

Result No.	Score	Query Match	Length	DB ID	Description
7	650	38.0	840	12	BG202940 RST22308
8	639.8	37.4	773	12	BG204962 RST24381
9	625	36.5	636	14	B0637986
10	618	36.1	770	12	BG195757
11	613.2	35.9	818	12	BG183776
12	599	35.0	600	14	BM819819
13	594	34.7	594	14	AA527298
14	590.8	34.5	794	12	BG571867 602593213
15	555	32.4	555	13	B1964101
16	555	32.4	804	12	BG203434
17	542.6	31.7	577	9	AI123712
18	539.2	31.5	724	9	AI1956432
19	538	31.4	540	13	B1964193
20	536.6	31.3	827	12	BG187447 RST6439 A
21	536.2	31.3	837	12	BG228003
22	528.8	30.9	1007	14	BQ958105
23	526.2	30.7	606	10	AM970720
24	525.6	30.7	897	12	BG185335
25	501.2	29.3	692	9	AI006567
26	499.2	29.2	525	12	BF924264
27	481.4	28.1	493	12	BF445897
28	479.8	28.0	631	12	BF784586
29	471.4	27.5	631	12	BF788496
30	467.4	27.3	703	10	BB649178
31	467	27.3	656	10	AW318621
32	459.4	26.8	635	10	BB572119
33	440.8	25.7	662	10	BB610546
34	435.8	25.5	445	9	AA992802
35	435.4	25.4	439	9	AI195138
36	423.4	24.7	425	9	AI393787
37	421.4	24.6	577	10	AV597266
38	416	24.3	417	10	BE220748
39	413.4	24.1	529	9	AA224157
40	397.8	23.2	402	9	AI265984
41	395.6	23.1	780	12	BG199309
42	395	23.1	395	9	AA992463
43	394.8	23.1	398	9	AI023643
44	390.8	22.8	395	9	AI024632
45	390.8	22.8	417	9	AI265978

ALIGNMENTS

RESULT 1
LOCUS BG186424 776 bp mRNA linear EST 21-APR-2001
DEFINITION RST5388 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG186424
VERSION BG186424.1 GI:13708111
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 776)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McGilligot,K., Booser,S., May,R., Smith,
E., Veloso,N., Kikka,A., Hess,J., Cothren,K., Lo,K., Offenbacher
J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE

JOURNAL MEDLINE
21227151
Contact: Scott J. Cain
Athersys, Inc.

COMMENT

3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 498.
Location/Qualifiers

FEATURES


```

source
1. .776
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="H1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is H1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in H1080 under normal circumstances."
BASE COUNT      220 a      156 c      165 g      234 t      1 others
ORIGIN

Query Match      43.9%; Score 751.8; DB 12; Length 776;
Best Local Similarity 99.6%; Pred. No. 2.3e-174;
Matches 764; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY  428  ATTCATTCATGCTCTCTGCGACCCACTTCAGCAATCAGAACAGTGGATTATCTTC 487
      |||||||
DB   1  ATTCATTCATGCTCTCTCTGCGACCCACTTCAGCAATCAGAACAGTGGATTATCTTC 60

OY  488  AGCAGTGTGAGACCAACATTTGAAACTCTTGATGTCATGACCTGATATTGGGGCC 547
      |||||||
DB   61  AGCAGTGTGAGACCAACATTTGAAACTCTTGATGTCATGACCTGATATTGGGGCC 120

OY  548  CCAGTATCAGGTGTATTTCTTCACCTTCAGCATGATGAGATGAGATGTTGAGAA 607
      |||||||
DB   121  CCAGTATCAGGTGTATTTCTTCACCTTCAGCATGATGAGATGAGATGTTGAGAA 180

OY  608  GTTATGTGACCTTATGACAAATGGCAACAGCTTCATGACATGATGATGATGATG 667
      |||||||
DB   181  GTTATGTGACCTTATGACAAATGGCAACAGCTTCATGACATGATGATGATGATG 240

OY  668  AAGGCAAAATCAGATACATCCAGCAATCATGCTGTGTAAGCTAGCCAAAGGGGATG 727
      |||||||
DB   241  AAGGCAAAATCAGATACATCCAGCAATCATGCTGTGTAAGCTAGCCAAAGGGGATG 300

OY  728  GTTGTGCTGGCAATGGGCATGGCGCTCTCCATGGGGGACCAACAGCTTCTCCACTT 787
      |||||||
DB   301  GTTGTGCTGGCAATGGGCATGGCGCTCTCCATGGGGGACCAACAGCTTCTCCACTT 360

OY  788  GCGAGATTCCTGCTCTTGAACATTAATATATATAGTATGATGATGATGATGATG 847
      |||||||
DB   361  GCGAGATTCCTGCTCTTGAACATTAATATATATAGTATGATGATGATGATGATG 420

OY  848  AAGACTGTAGCTGAGCTGATTTGTACGATCTGAGGACATTTAAAGTTGAGGGTTTAC 907
      |||||||
DB   421  AAGACTGTAGCTGAGCTGATTTGTACGATCTGAGGACATTTAAAGTTGAGGGTTTAC 480

OY  908  ATTCCTATATCAAAAATATATGTTGTGCAATGTTGTTCAGCGTACAGGTAACCAATA 967
      |||||||
DB   481  ATTCCTATATCAAAAATATATGTTGTGCAATGTTGTTCAGCGTACAGGTAACCAATA 540

OY  968  TGTGACAAATCAGGGGCTCAGAGAAATCAACCAAAAATAGCTCTCAGATGACCTT 1027
      |||||||
DB   541  TGTGACAAATCAGGGGCTCAGAGAAATCAACCAAAAATAGCTCTCAGATGACCTT 600

OY  1028  GACTTAATATACAGCATCTTATCTCTTCTGCGACCTTAAGATATATCTCTCTC 1087
      |||||||
DB   601  GACTTAATATACAGCATCTTATCTCTTCTGCGACCTTAAGATATATCTCTCTC 660

OY  1088  TGAGCGAGTGTGAATATTTTCTATCAGAGATGATGATGATGATGATGATGATG 1147
      |||||||
DB   661  TGAGCGAGTGTGAATATTTTCTATCAGAGATGATGATGATGATGATGATGATG 720

OY  1148  CTCCTCTTAAATTAATACAGTTTCAGGAACCCCTGAAGTTTAA 1194
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DB   721  CTCCTCTTAAATTAATACAGTTTCAGGAACCCCTGAAGTTTAA 766

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RESULT 2
BG186928/c

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LOCUS      BG186928      874 bp      mRNA      linear      EST 21-APR-2001
DEFINITION RSTS905 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG186928
VERSION    BG186928.1  GI:13708615
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 874)
            Harrington,J.V., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,
            E., Veloso,N., Kliska,A., Hess,J., Cothren,K., Lo,K., Offenbacher,
            J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL    2127151
MEDLINE    Contact: Scott J. Cain
COMMENT    Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@atersys.com
            High quality sequence stop: 522.
            Location/Qualifiers
            1. 874
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="Athersys RAGE Library"
               /cell_line="H1080"
               /note="See 'Creation of Genome-wide Protein Expression
               Libraries using Random Activation of Gene Expression',
               Nature Biotechnology, in press. Note that even though the
               cell type indicated is H1080, since a random activation
               method was used, these sequence tags are not necessarily
               expressed in H1080 under normal circumstances."
BASE COUNT      276 a      168 c      162 g      268 t
ORIGIN

Query Match      43.4%; Score 743.4; DB 12; Length 874;
Best Local Similarity 94.7%; Pred. No. 2.8e-172;
Matches 802; Conservative 0; Mismatches 41; Indels 4; Gaps 3;

OY  843  TGGGGAAGACTTGATGCTGAGCTGATTTGTACATCTGAGGAACATTAAGTTGAGGCT 902
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DB   856  TTGGGGAACCTAGTAGCTGAGTTAATTTGT--CCTTTTGGGAACATTAAGTTGAGGCT 799

OY  903  TTTACATTTGCTGATTAACAAAATATTTGTTGCAATGTTTGCAGCTACAGSTA-CAC 961
      |||||
DB   798  TTTACATTTGCTGATTAACAAAATATTTGTTGCAATGTTTGCAGCTACAGSTA-CAC 739

OY  962  CAATTAATGTTGACAAATTCAGGGGCTCAGAGAAATCAACCAAAAATAGTCTCTCAGAT 1021
      |||||
DB   738  CAATTAATGTTGACAAATTCAGGGGCTCAGAGAAATCAACCAAAAATAGTCTCTCAGAT 680

OY  1022  GACTTAATATATCTCAGCATCTTATCAGCTTCTCTGCGACCTTAAGATATAT 1081
      |||||
DB   679  GACTTAATATATCTCAGCATCTTATCAGCTTCTCTGCGACCTTAAGATATAT 620

OY  1082  CTCCTCTGAGCGAGTGTGAATATTTTCTATCAGAGATGATGATGATGATGATG 1141
      |||||
DB   619  CTCCTCTGAGCGAGTGTGAATATTTTCTATCAGAGATGATGATGATGATGATG 560

OY  1142  TGACTACTGCTTTTAATTAATACAGTTTTCAGGAACCCCTGAAGTTTAAAGTTAT 1201
      |||||
DB   559  TGACTACTGCTTTTAATTAATACAGTTTTCAGGAACCCCTGAAGTTTAAAGTTAT 500

OY  1202  TATCTCTTAATACATTTGAGAGATGATGATGATGATGATGATGATGATGATG 1261
      |||||
DB   499  TATCTCTTAATACATTTGAGAGATGATGATGATGATGATGATGATGATGATG 440

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1262 AGGGGACTAGTGCCTTATAGCTAATTAGTCCCTCCGTCAGCTTGA 1321
|||||
439 AGGGGACTAGTGCCTTATAGCTAATTAGTCCCTCCGTCAGCTTGA 380
|||||
1322 CCGTTCCTTTGATCCACAATAATACATTAAACCTGTAATTCATATGTTT 1381
|||||
379 CCGTTCCTTTGATCCACAATAATACATTAAACCTGTAATTCATATGTTT 320
|||||
1382 AAGGTAATAGATTTAGTATTAATAGTCCGTAATGCTGTAATTTCTGTA 1441
|||||
319 AAGGTAATAGATTTAGTATTAATAGTCCGTAATGCTGTAATTTCTGTA 260
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1442 TGTTCCTCCCATCGCCCACTTGGATGTCAGAGGTTGAGTTGATTTA 1501
259 TGTTCCTCCCATCGCCCACTTGGATGTCAGAGGTTGAGTTGATTTA 200
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1502 ACAATGTCATAAATATCTATAGAGTACAGTCCCAATGATATTCAAATGTCATGT 1561
199 ACAATGTCATAAATATCTATAGAGTACAGTCCCAATGATATTCAAATGTCATGT 140
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1562 TGACCAAGAGGATTTTATATCTGAACAATACATTAATTAATACCTTAGAGAA 1621
139 TGACCAAGAGGATTTTATCTGAACAATACATTAATTAATACCTTAGAGAA 80
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1622 TTTTGACCTGGCTTTGATTAATACTGTGCAAGAAATGTAATGACATATATGAAA 1681
79 TTTTGACCTGGCTTTGATTAATACTGTGCAAGAAATGTAATGACATATATGAAA 20
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1682 TAAACAC 1688
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19 TAAACAC 13
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RESULT 3
BM924169 1103 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6630525 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760396
DEFINITION 5', mRNA sequence.
ACCESSION BM924169
VERSION BM924169.1 GI:19374548
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1103)
REFERENCE
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM12807 row: f column: 13
High quality sequence stop: 564.
Location/Qualifiers
1..1103
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/db_xref="taxon:9606"
/clone="IMAGE:5760396"
/clone_1ib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo female kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH-MGC Library.

BASE COUNT 274 a 285 c 279 g 264 t 1 others

ORIGIN

Query Match 41.1%; Score 704.4; DB 14; Length 1103;
Best Local Similarity 91.9%; Pred. No. 1.2e-162;
Matches 858; Conservative 0; Mismatches 56; Indels 20; Gaps 10;

27 CTGAGACTGCTGCTCTCTCTCTGAGAGAGAGCTGAGGCTGTTGAGAAATCCTTTGGA 86
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1 CTGAGCTCTGCTGCTCTCTCTCTGAGAGAGAGCTGAGGCTGTTGAGAAATCCTTTGGA 60
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87 GCGAGCTCATCTATTTGGCAACCTGCTGCTTTGTTTCTCTCTCTCTCTCTCTGTCAG 146
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61 GCGAGCTCATCTATTTGGCAACCTGCTGCTTTGTTTCTCTCTCTCTCTCTCTGTCAG 120
|||||
147 ATGAATACATGAGTCTCCACAAACCGGAGGAGTACCCCGAGCTGAGTAAGTGTGTC 206
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121 ATGAATACATGAGTCTCCACAAACCGGAGGAGTACCCCGAGCTGAGTAAGTGTGTC 180
|||||
207 ATGAGACTACAGCTTTCGAGGCTACCAAGGCCCTGAGGCGGAGGCTCTCTGCA 266
|||||
181 ATGAGACTACAGCTTTCGAGGCTACCAAGGCCCTGAGGCGGAGGCTCTCTGCA 240
|||||
267 TTCAGAGAAACCATGGAACATGGAACATGGAACATGGAACATGGAACATGGAACATG 326
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241 TTCAGAGAAACCATGGAACATGGAACATGGAACATGGAACATGGAACATGGAACATG 300
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327 GTGAGAGAGGCGCAAAAGTGAGCTGGGCTCTGAGGAGGAGGCGGCGGAGGAGGCGGCA 386
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301 GTGAGAGAGGCGCAAAAGTGAGCTGGGCTCTGAGGAGGAGGCGGCGGAGGAGGCGGCA 360
|||||
387 AAGGAGAGAGGCGCTACCGGCGGATTCACCAAGCTTCAGTATGCTATGCTCTCTC 446
|||||
361 AAGGAGAGAGGCGCTACCGGCGGATTCACCAAGCTTCAGTATGCTATGCTCTCTC 420
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447 TGCGAACCCCATTCAGCAATCAGACAGTGGGATTCCTTCAGCAGTGTGGAGACACA 506
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421 TGCGAACCCCATTCAGCAATCAGACAGTGGGATTCCTTCAGCAGTGTGGAGACACA 480
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507 TTGGAACCTTCTGATGTCATGCTGATGATTTGGGCGGCGGAGTTCAGGCTGAT 566
|||||
481 TTGGAACCTTCTGATGTCATGCTGATGATTTGGGCGGCGGAGTTCAGGCTGAT 540
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567 TCTTCACCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 626
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627 A-CAGTGGCAACAGAGCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATG 684
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601 ACCAATGGCAACAGAGCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATG 660
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685 ATCCAGCATGATGCT--TGCTGGAAGCT--AGCAAGGAGGATGAGTTT--GGCTGCA 739
|||||
661 ATCCAGCATGATGCTGCTGCTGGAAGCTTAACCAAGGAGGATGAGTTTGGGTGCGAA 720
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740 ATGGGCAATGGGCTCTCCATGGGAGCCACCAAGGCTCT--CCACCTTGGAGATTC 796
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721 ATGGGCAATGGGCTCTCCATGGGAGCCACCAAGGCTCTCTCCACCTTGGAGATTC 780
|||||
797 CTGCTCTTTCAGAACTAGTAATATA--TGACTAGAAATAGCTCAGCTTTGGG--AAG 850
|||||
781 CTGCTCTTTCAGAACTAGTAATATAATATGCTTGAATAGCTCCCGCTTGGGGAAGAC 840
|||||
851 ACTTGTAGCTGAGCTGATTTGTTAGCATC--TGAGGAACATTAAGTGAAGGCTTTTACA 908
|||||
841 ACTGAACCTGAGGCTGAGCTTGGCTCCGACCTGAGGGAACATTAAGTGAAGGCTTTTACA 900
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909 --TTGCTGATTCAAAAAATTTATGTTGCAATG 940

Db	901	CTTGCTGACTCAAAATTAATCTTGGAG	934
RESULT 4			
LOCUS	BG201468	762 bp	mRNA linear EST 21-APR-2001
DEFINITION	RS120685 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BG201468		
VERSION	BG201468.1	GI:13723043	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 762)		
	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith,E., Veloso,N., Kikka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.		
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression		
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)		
MEDLINE	21227151		
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scaine@atersys.com		
FEATURES	High quality sequence stop: 504.		
	Location/Qualifiers		
source	1. 762 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."		
BASE COUNT	218 a 154 c 162 g 228 t		
ORIGIN			
Query Match	40.5%: Score 692.6; DB 12; Length 762;		
Best Local Similarity	98.3%: Pred. NO. 8.8e-160;		
Matches 742:	Conservative 0; Mismatches 9; Indels 4; Gaps 4;		
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Db	1 ATGGATTCATGCGCTTCTCTGCGAACCCACTTCAGCAATCAGACAGTGGATATATCTTC	60	
OY	488 AGCACTGTTGAGACACAAATTGGAACCTCTTGATGATCATGATCGTGAATTTGGGGCC	547	
Db	61 AGCATGTTGAGACACAAATTGGAACCTCTTGATGATCATGATCGTGAATTTGGGGCC	120	
OY	548 CCAGTATCAGGTGTATTTCTTCACCTTCAGCATGATGAAACATGAGATGTTGAGAA	607	
Db	121 CCAGTATCAGGTGTATTTCTTCACCTTCAGCATGATGAAACATGAGATGTTGAGAA	180	
OY	608 GGTGATGTTGATCTTATGACAAATGGCAACAGCTTCAGCATGATGAAACATGAGATGTTGAGAA	667	
Db	181 GGTGATGTTGATCTTATGACAAATGGCAACAGCTTCAGCATGATGAAACATGAGATGTTGAGAA	240	
OY	668 AAGGCAAAATCAGATACATCCAGCAATATATGCTGTGCTGAAGCTGAGCCAAAGGGATGAG	727	
Db	241 AAGGCAAAATCAGATACATCCAGCAATATATGCTGTGCTGAAGCTGAGCCAAAGGGATGAG	300	
OY	728 GTTTGGCTGCGAATGGCAATGGCGCTTCATGGGGACACCAACGCTTCTCCACTTT	787	

Db	301	GTTTGGCTGCGCAATGGGCAATGGCCCTCCATGGGGGACCACCAACCGCTTCCACCTTT	360
Oy	788	CGAGGATTCCTGCTCTTTGGAACATAGTAATATATATGACTAGAAATAGCTCCACTTTGGGG	847
Db	361	GCAGGATTCCTGCTCTTTGGAACATAGTAATATATATGACTAGAAATAGCTCCACTTTGGGG	420
Oy	848	AAGACTTGTAGCTGAGCTGATTTGTTTACGATCTGAGAACTTAAAGTTGAGGGTTTAC	907
Db	421	AAGACTTGTAGCTGAGCTGATTTGTTTACGATCTGAGAACTTAAAGTTGAGGGTTTAC	480
Oy	908	ATTGCTGATTCGAAAAAATATATGTTGGTTCGAAATGTTGTTCAAGCTACAGCTACCAATTA	967
Db	481	ATTGCTGATTCGAAAAAATATATGTTGGTTCGAAATGTTGTTCAAGCTACAGCTACCAATTA	540
Oy	968	TGTTGGACAATTCAGGGGCTCAGAGAATTCACACCAAAATATGTTTCTGAGATGACTT	1027
Db	541	TGTTGGACAATTCAGGGGCTCAGAGAATTCACACCAAAATATGTTTCTGAGATGACTT	600
Oy	1028	GACTAATATATACACCACTTATATACACTTTCCTTGGACCTTAACATATATGTTCCG	1087
Db	601	GACTAATATATACACCACTTATATACACTTTCCTTGGACCTTAACATATATGTTCCG	660
Oy	1088	TGACCCAGGTTGGAAATATTTTTTTTCTATCAGAGAATCATTTTGGCAAGAAATTTTGACTA	1147
Db	661	TGACCCAGGTTGGAAATATTTTTTTTCTATCAGAGAATCATTTTGGCAAGAAATTTTGACTA	717
Oy	1148	CTCTGCTTTTAAATTAATATACAGTTTTCAGGAACC	1182
Db	718	CTCTGCTTTT-ATTAAATACAGTTTTCAGGAACC	751
RESULT 5			
LOCUS	828 bp	mRNA	linear
DEFINITION	60246452P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592701 5',		
ACCESSION	BC400260		
VERSION	BC400260.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 828)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@bbs.femail.nih.gov Tissue Procurement: Clontech Laboratories, Inc. cDNA Library Preparation: Clontech Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L10CM1331 row: h column: 14 High quality sequence stop: 740. Location/Qualifiers 1. 828 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4592701" /clone_1id="NIH_MGC_75" /lab_host="DH10B (TI phage-resistant)" /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: Site_1 (99ccgctcgcgc); Site_2: Site_1 (99ccatcgcgc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATATGAGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCAGCGCCGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 clones contained inserts by PCR. This library was enriched for full-length clones		

Db 421 CAGCAGTGTGAGACCAACATTTGAAACTCTTTGATGTCATGACTGTAGATTGGGCG 480
Qy 547 CCCAGTATCAGGCTGATTTCTTCACCTTCAGATGATGAGCATGAGATGTGAGGA 606
Db 481 CCCAGTATCAGGCTGATTTCTTCACCTTCAGATGATGAGCATGAGATGTGAGGA 540
Qy 607 AGTGTATGTGATCTTATGACATGAGCAACAGCTCTTCACATGATCAGCTATGAAT 666
Db 541 AGTGTATGTGATCTTATGACATGAGCAACAGCTCTTCACATGATCAGCTATGAAT 600
Qy 667 GAGGCGCAATATGATATCAGATCCAGCATATGCTGTCTG -AAGTATGCAAGGGATG 725
Db 601 GAGGCGCAATATGATATCAGATCCAGCATATGCTGTCTG -AAGTATGCAAGGGATG 660
Qy 726 AGCTTGGCTGGATGAGGCAATGGGCGCTTCATGGGACCAAGCTTCCTCAGCT 785
Db 661 GAGCTGTGGTGGATGAGGCAATGGGCGCTTCATGGGACCAAGCTTCCTCAGCT 718
Qy 786 TTGCAGATATTCCTCTTTGAAACTAAGTAATATATGATAGATAGCTTCACCTTTGG 845
Db 719 TTGCAGATATTCCTCTTTGAAACTAAGTAATATATGATAGATAGCTTCGA -TTTGG 777
Qy 846 GGAAGACTTGTAGCTGAGCTGATTTGTTCAGATCTGAGG 884
Db 778 GGAAGACTTGTAG -TGAGCTGA -TTGTTACGATCTGAGG 814

RESULT 7
Bg202940/c 840 bp mRNA linear EST 21-APR-2001
LOCUS RST22308 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION Bg202940
VERSION Bg202940.1 GI:13724627
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 840)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
'E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J., and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com
High quality sequence stop: 542.
location/Qualifiers
1. 840
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression'
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 256 a 154 c 161 g 268 t 1 others
ORIGIN

Query Match 38.0%; Score 650; DB 12; Length 840;
Best Local Similarity 97.2%; Pred. No. 2.8e-149;
Matches 693; Conservative 0; Mismatches 16; Indels 4; Gaps 3;

Qy 977 ATTGAGGGGCTCAGAGAATCAACCAAAATAGCTTCTCAGATGACTGACTATAT 1036
Db 718 AATTGGGGGCTCAGAGAATCAACCAAAATAGCTTCTCAGATGACTGACTATAT 660
Qy 1037 ACTGAGCATCTTTATCTCTTTCTTGGACCTAAAGATATTCCTCTGAGCAGG 1096
Db 659 ATACAGCATCTTTTACCTCTTCCCTGGACATAAAGAT -ATTTCTCTGAGCAGG 601
Qy 1097 TTGGAATATTTTTTTCTATCAGACATGATTTGCAAGATTTTGATCTCTCTT 1156
Db 600 TTGGCAATATTTTTTTCTATCAGACATGATTTGCAAGATTTTGATCTCTCTT 541
Qy 1157 TAATTTATACAGTTTTCAGAACCCCTGAGATTTTAACTTATCTTTAAAT 1216
Db 540 TAATTTATACAGTTTTCAGAACCCCTGAGATTTTAACTTATCTTTAAAT 481
Qy 1217 TTGAGAGATCGGATGATGATATGAGAGGCTGGGCAAGACAGGGGCACTAGCTGC 1276
Db 480 TTGAGAGATCGGATGATGATATGAGAGGCTGGGCAAGACAGGGGCACTAGCTGC 421
Qy 1277 CTATTATCTAATTTAGTGCCTCGCTGTTACGCTTACGCTTTCCTTTTGA 1336
Db 420 CTATTATCTAATTTAGTGCCTCGCTGTTACGCTTACGCTTTCCTTTTGA 361
Qy 1337 CCACAAATPACATTTAAACTGTAATGATACATACATGCTATTTTAACTATAGATT 1396
Db 360 CCACAAATPAC - -AAACTGTAATGATACATACATGCTATTTTAACTATAGATT 303
Qy 1397 TAGCTATTAAGTGTGACACAGTATGCTGTTGTAATTTTGTATGTTGCTCCACATCG 1456
Db 302 TAGCTATTAAGTGTGACACAGTATGCTGTTGTAATTTTGTATGTTGCTCCACATCG 243
Qy 1457 CCCCCAAGCTTGGATGTGGGGTCAAGAGGTTGAGTTCACTTTTAAACAATGTCAATAAT 1516
Db 242 CCCCCAAGCTTGGATGTGGGGTCAAGAGGTTGAGTTCACTTTTAAACAATGTCAATAAT 183
Qy 1517 ATCTCATGAGCTAGTACAGTGCCTAATGATATTCAAATGTCATGTTGACAGAGGATTT 1576
Db 182 ATCTCATGAGCTAGTACAGTGCCTAATGATATTCAAATGTTGATGTTGACAGAGGATTT 123
Qy 1577 TATATCTGAGAGCAATACATATTAATTAATACCTTAGAGAAAGATTTGACCTGCTTT 1636
Db 122 TATATCTGAGAGCAATACATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 63
Qy 1637 AGATTAACCTGTGGCAAGAAATATGATGACATATTTGGAATTAACACA 1689
Db 62 AGATTAACCTGTGGCAAGAAATATGATGACATATTTGGAATTAACACA 10

RESULT 8
Bg204962 773 bp mRNA linear EST 21-APR-2001
LOCUS RST24381 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION Bg204962
VERSION Bg204962.1 GI:13726649
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 773)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
'E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J., and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@ethersys.com
High quality sequence stop: 398.

FEATURES

SOURCE

1. 773
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 218 a 150 c 171 g 234 t

ORIGIN

Query Match 37.4%; Score 639.8; DB 12; Length 773;

Best Local Similarity 94.7%; Pred. No. 9e-147; Indels 8; Gaps 5;

Matches 717; Conservative 0; Mismatches 32;

OY 428 ATTGATTCATGCTCTCTGGCAACCCACTTCAGCAATCAGAAAGTGGATTATCTTC 487
|||||
DB 1 ATTGATTCATGCTCTCTCTGGCAACCCACTTCAGCAATCAGAAAGTGGATTATCTTC 60
OY 488 AGCACTGTTGAGACCAACATTGGAACCTTCTTGGATGTCATGCTGATGATTTGGGCC 547
|||||
DB 61 ACAGAGCTTGAGACCAACATTGGAACCTTCTTGGATGTCATGCTGATGATTTGGGCC 120
OY 548 CCAGATTCAGGCTGATTTCTTCCACCTTCAGCAATGAGCATGAGCATGTTGAGAA 607
|||||
DB 121 CCAGATTCAGGCTGATTTCTTCCACCTTCAGCAATGAGCATGAGCATGTTGAGAA 180
OY 608 GTGATGTTGATCTTATGCAATGAGCAACACAGTCTTCAGCATGATGATGATGAAATG 667
|||||
DB 181 GTGATGTTGATCTTATGCAATGAGCAACACAGTCTTCAGCATGATGATGATGAAATG 240
OY 668 AAGGCAATTCAGATTCATCCAGCAATCATGCTGCTCAGTACAGCAAGGAGATGAG 727
|||||
DB 241 AAGGCAATTCAGATTCATCCAGCAATCATGCTGCTCAGTACAGCAAGGAGATGAG 300
OY 728 GTTGGCTGCAATGAGGCAATGAGGCTCTCCAGTGGGACACCAAGCTCTCCACCTTT 787
|||||
DB 301 GTTGGCTGCAATGAGGCAATGAGGCTCTCCAGTGGGACACCAAGCTCTCCACCTTT 360
OY 788 GCAGATTCCTGCTCTTAACTAAGTAATATATGATAGATAGCTCCACTTTGGGG 847
|||||
DB 361 GCAGATTCCTGCTCTTAACTAAGTAATATATGATAGATAGCTCCACTTTGGGG 420
OY 848 AAGACTTGTAGCTGAGCTGATTTGTAGCATCTGAGGAACATTAAAGTTGAGGTTTAC 907
|||||
DB 421 AAGACTTGTAGCTGAGCTGATTTGTAGCATCTGAGGAACATTAAAGTTGAGGTTTAC 480
OY 908 ATTGCTGATTCAGAAATTTATGTTGCAATGTTGTCACGCTACAGGATGACCATATA 967
|||||
DB 481 ATTGCTGATTCAGAAATTTATGTTGCAATGTTGTCACGCTACAGGATGACCATATA 540
OY 968 TG-TTGGAAATTCAGGGGCTCAGAGAAATCAACCAAAAT-AGTCTTTCAGATGAGC 1025
|||
DB 541 TGTGTTGACCATTCAGGGGCTCAGAGAAATCAACCAAAATAGTCTTTCAGATGAGC 600
OY 1026 TTGACTAATATATCTGAGCATCTTTATCACTCTTCTGGACCTAAAGATATCTCC 1085
|||||
DB 601 TTGACTAATATATCTGAGCATCTTTATCACTCTTCTGGACCTAAAGATATCTCC 658
OY 1086 TGTGAGCAGGTTGAAATTTTCTTCTACAGAAAGTCAATTTGCAAGATTTTGAC 1145
|||||
DB 659 TGTGAGCAGGTTGAA--ATTTTCTTCTTATATACAGAAAGCAATTTGCAAGATTTGACT 716
OY 1146 TACTCTGCTTTTAAATTAATACAGTTTTCAGGAACC 1182

DB 717 GGTTCG--TTTAAATTAATACAGGCTTAAGAACCC 751

RESULT 9

LOCUS

DEFINITION

B0637986 636 bp mRNA linear EST 15-JUL-2002
hd17a10.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 17 row: a column: 10
Seq primer: M13RP1 reverse primer (Abi).
Location/Qualifiers
1. 636
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="hd17a10"
/clone_lib="Human Retina cDNA (Un-normalized, unamplified)
): hd/he"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMD108"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor [5'-pGACTGTGTTTAAATGCGGCGGCCGCC(7)15-3'
]. EST analysis was performed on the unamplified library
at the NIH Intramural Sequencing Center (NISC)."

FEATURES

SOURCE

BASE COUNT

155 a 156 c 177 g 148 t
Query Match 36.5%; Score 625; DB 14; Length 636;
Best Local Similarity 100.0%; Pred. No. 3.9e-143;
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 CAGGCTCCGAGCTCTGCTGCTTCTCAGGGAGCTGAGGCTGTTGAGAAATCATG 79
|||||
DB 12 CAGGCTCCGAGCTCTGCTGCTTCTCAGGGAGCTGAGGCTGTTGAGAAATCATG 71
OY 80 CTTTGAGGAGCTCATCTATTTGCAACTGCTGCTTTGTTTCTCCCTTTTGGCTG 139
|||||
DB 72 CTTTGAGGAGCTCATCTATTTGCAACTGCTGCTTTGTTTCTCCCTTTTGGCTG 131
OY 140 TGTCAAGATGAATATGAGCTCTCCACAACCGAGAGCTACCCAGAGCTCAGTAAG 199
|||||
DB 132 TGTCAAGATGAATATGAGCTCTCCACAACCGAGAGCTACCCAGAGCTCAGTAAG 191

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QY 200 TGTGTCAGAGACCTACAGCTTTGAGGCTACCAAGGCCCCCTGGGCCACCGGCCCT 259
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Db 192 TGTGTCATGAGACCTACAGCTTTGAGGCTACCAAGGCCCCCTGGGCCACCGGCCCT 251
    |||||||
QY 260 CCTGCAATTCAGAGAAACATGGAACATGCAACATGAGCACTGGTCATGAAGA 319
    |||||||
Db 252 CCTGCAATTCAGAGAAACATGGAACATGGAACATGAGCACTGGTCATGAAGA 311
    |||||||
QY 320 GCCAAGCTGAGAAAGGCGCAAAAGTGACCTGGGCTTGAGGGGAGCGGGGACCAT 379
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Db 312 GCCAAGCTGAGAAAGGCGCAAAAGTGACCTGGGCTTGAGGGGAGCGGGGACCAT 371
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QY 380 GGGCCCAAGAGAGAGGAGGCTACCGGGGATTCACAGCACTTCAGATTCATTCATG 439
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Db 372 GGGCCCAAGAGAGAGGAGGCTACCGGGGATTCACAGCACTTCAGATTCATTCATG 431
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QY 440 GCTTCTCTGGCAACCCATTCAGCAATCAGAGAGTGAGATTCCTTCAGCAGTGTGAG 499
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Db 432 GCTTCTCTGGCAACCCATTCAGCAATCAGAGAGTGAGATTCCTTCAGCAGTGTGAG 491
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QY 500 ACCAACAATTGGAACCTTTGATGTCATGACGTGATGATTTGGGGCCCAATATCAGGT 559
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Db 492 ACCAACAATTGGAACCTTTGATGTCATGACGTGATGATTTGGGGCCCAATATCAGGT 551
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QY 560 GTGATTTCTTCACTTCAGCATGATGATGATGATGATGATGATGATGATGATGATG 619
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Db 552 GTGATTTCTTCACTTCAGCATGATGATGATGATGATGATGATGATGATGATGATG 611
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QY 620 CTTATGCACATGCAACAGATCT 644
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Db 612 CTTATGCACATGCAACAGATCT 636
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RESULT 10
BG195757 770 bp mRNA linear EST 21-APR-2001
LOCUS RST14951 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG195757
ACCESSION BG195757.1 GI:13717444
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens

```

```

REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
E., Veloso,N., Kijka,A., Hess,J., Cochren,K., Lo,K., Offenbacher
J., Danzig,J. and Ducar,M.

```

```

TITLE Creation of genome-wide protein expression libraries using random
activation of genome-wide protein expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 386.
Location/Qualifiers
1..770
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of genome-wide protein expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily

```

FEATURES

```

source
1..770
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of genome-wide protein expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily

```

```

BASE COUNT 220 a 157 c 162 g 231 t
ORIGIN
Query Match 36.1% Score 618; DB 12; Length 770;
Best Local Similarity 96.6%; Pred. No. 2.1e-141;
Matches 663; Conservative 0; Mismatches 20; Indels 3; Gaps 3;

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QY 428 ATTGCATTCATGCGCTTCTCTGCAACCCATTCAGCAATCAGAACATGCGGATATTC 487
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Db 1 ATTGCATTCATGCGCTTCTCTGCAACCCATTCAGCAATCAGAACATGCGGATATTC 60
    |||||||
QY 488 AGCAGTGTGAGACCAACATGGAACCTCTTGATGTCATGACGAGATGAGATTTGGGCC 547
    |||||||
Db 61 AGCAGTGTGAGACCAACATGGAACCTCTTGATGTCATGACGAGATGAGATTTGGGCC 120
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QY 548 CCAATATCAGGCTGTGATTTCTTCACTTCAGCATGATGATGATGATGATGATGATGATG 607
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Db 121 CCAATATCAGGCTGTGATTTCTTCACTTCAGCATGATGATGATGATGATGATGATGATG 180
    |||||||
QY 608 GTGATGTGTACCTTATGCAACATGCAACACAGTCTTCAGCATGTACAGTATGAATG 667
    |||||||
Db 181 GTGATGTGTACCTTATGCAACATGCAACACAGTCTTCAGCATGTACAGTATGAATG 240
    |||||||
QY 668 AAGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727
    |||||||
Db 241 AAGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
    |||||||
QY 728 GTTGGCTGCGAATGAGGCAATGAGGCTCTCCATGGGACCAACAGCTTCTCCACCTTT 787
    |||||||
Db 301 GTTGGCTGCGAATGAGGCAATGAGGCTCTCCATGGGACCAACAGCTTCTCCACCTTT 360
    |||||||
QY 788 GCAGGATTCCTGCTCTTTGAAACTAGTAATATATGATGATGATGATGATGATGATG 847
    |||||||
Db 361 GCAGGATTCCTGCTCTTTGAAACTAGTAATATATGATGATGATGATGATGATGATG 420
    |||||||
QY 848 AAGACTGTAGCTAGCTGATTTGTTAGATCTGAGCAATTAAGTGTAGGCTTTTAC 907
    |||||||
Db 421 AAGACTGTAGCTAGCTGATTTGTTAGATCTGAGCAATTAAGTGTAGGCTTTTAC 480
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QY 908 ATTGCTGATTCACCAAAATTAAT--GTTGCAATTTGTTACGCTACAGTACCAATA 966
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Db 481 ATTGCTGATTCACCAAAATTAATTTGGTTGCAATTTGTTACGCTACAGTACCAATA 540
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QY 967 ATGTGACCAATTCAGGGGCTCAGAGAACATCACCAAAATAGCTTTTCAGATGACCT 1026
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Db 541 ATGTGACCAATTCAGGGGCTCAGAGAACATCACCAAAATAGCTTTTCAGATGACCT 600
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QY 1027 TGACTAATATACACGATCTTTATCACTCTTCCCTGGGACCAAAAGATAATTCCT 1086
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Db 601 TGACTAATATACACGATCTTTATCACTCTTCCCTGGGACCAAAAGATAATTCCT 658
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QY 1087 CTGACGAGGTTGGAATATTTT 1112
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Db 659 CATGCCGCGGTGGAATTTT 684
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```

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RESULT 11
BG183776 818 bp mRNA linear EST 21-APR-2001
LOCUS RST2684 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG183776
ACCESSION BG183776.1 GI:13705463
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
E., Veloso,N., Kijka,A., Hess,J., Cochren,K., Lo,K., Offenbacher

```


plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library.

BASE COUNT 165 a 109 c 122 g 159 t
ORIGIN

Query Match 32.4%: Score 555; DB 13; Length 555;

Best Local Similarity 100.0%; Pred. No. 6.7e-126;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 582 TGATGAAGCATGAGAGTGTGAGAGTGTATGTACTTATGCACATGCAACACAG 641
|||
Db 1 TGATGAAGCATGAGAGTGTGAGAGTGTATGTACTTATGCACATGCAACACAG 60
QY 642 TCTTCAGCATGTACAGCTATGAAATGAAGGCAATCAGATACATCCAGCATGCTG 701
|||
Db 61 TCTTCAGCATGTACAGCTATGAAATGAAGGCAATCAGATACATCCAGCATGCTG 120
QY 702 TGCCTGAAGCTAGCCAAAGGGATGAGTTTGGCTGCGAATGGCAATGGCGCTCTCCATG 761
|||
Db 121 TGCCTGAAGCTAGCCAAAGGGATGAGTTTGGCTGCGAATGGCAATGGCGCTCTCCATG 180
QY 762 GGGACCAACACGCTTCTCCACCTTTGCGAGATTCCTCTTGAACCTAAGTAATAT 821
|||
Db 181 GGGACCAACACGCTTCTCCACCTTTGCGAGATTCCTCTTGAACCTAAGTAATAT 240
QY 822 ATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGTGTGTTACGATCG 881
|||
Db 241 ATGACTAGAAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGTGTGTTACGATCG 300
QY 882 AGGAACATTAAGTTGAGGGTTTACATGCTGTATTCAAAATATATGTTGCAATGT 941
|||
Db 301 AGGAACATTAAGTTGAGGGTTTACATGCTGTATTCAAAATATATGTTGCAATGT 360
QY 942 TGTTCACGCTACAGGTACCAATATGTTGACAAATTCAGGGCTCAGAGAATCAACC 1001
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QY 1002 ACAAAATAGTCTTCAGATGACCTTGACTAATATACACATCTTATCAGCTTTCC 1061
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Db 421 ACAAAATAGTCTTCAGATGACCTTGACTAATATACACATCTTATCAGCTTTCC 480
QY 1062 TTGCACCTAAAGATATTTCTCTGACGACAGTTGGAATATTTTTTCTATCACAG 1121
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Db 481 TTGCACCTAAAGATATTTCTCTGACGACAGTTGGAATATTTTTTCTATCACAG 540
QY 1122 AAGTCATTTGCAAG 1136
|||
Db 541 AAGTCATTTGCAAG 555

Search completed: January 15, 2003, 19:31:52
Job time : 2259 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 17:17:45 : Search time 83 Seconds

(without alignments)
6325.670 Million cell updates/sec

Title: US-10-036-041-1

Perfect score: 1712

Sequence: 1 ggcacatgcggcggagagacc.....ttgttaagaataaaaaaa 1712

Scoring table: IDENTITY_MUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by the change to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696.2	40.7	1123	3	US-09-188-930-28 Sequence 28, Appl
2	696.2	40.7	1123	3	US-09-188-930-203 Sequence 203, Appl
3	78.8	4.6	3275	4	US-09-370-838-151 Sequence 151, App
4	74.6	4.4	1313	2	US-08-463-911-6 Sequence 6, Appl
5	74.6	4.4	4517	4	US-09-140-804-9 Sequence 9, Appl
6	72.8	4.3	1868	1	US-08-392-367B-1 Sequence 1, Appl
7	72.8	4.3	1868	1	US-08-893-467A-1 Sequence 1, Appl
8	70.4	4.1	1276	2	US-08-463-911-1 Sequence 1, Appl
9	68	4.0	1560	2	US-08-794-795-5 Sequence 5, Appl
10	68	4.0	1560	4	US-09-249-200-5 Sequence 5, Appl
11	66.4	3.9	1703	2	US-08-794-795-1 Sequence 1, Appl
12	66.4	3.9	1703	4	US-09-249-200-1 Sequence 1, Appl
13	63.6	3.7	729	4	US-09-140-804-10 Sequence 10, Appl
14	61.8	3.6	750	3	US-09-188-930-19 Sequence 19, Appl
15	61.8	3.6	1107	3	US-09-188-930-217 Sequence 217, App
16	60.2	3.5	1560	4	US-09-453-702B-264 Sequence 264, App
17	60.2	3.5	61663	4	US-09-453-702B-62 Sequence 62, App
18	59	3.4	1341	2	US-08-945-848-7 Sequence 7, Appl
19	59	3.4	2363	4	US-08-945-848-6 Sequence 6, Appl
20	58	3.4	5102	1	US-08-494-168-1 Sequence 1, Appl
21	57.2	3.3	1572	4	US-09-297-269-39 Sequence 39, Appl
22	56.6	3.3	653	4	US-09-336-536-32 Sequence 32, Appl
23	56.6	3.3	843	4	US-09-118-408-23 Sequence 23, Appl
24	56.6	3.3	843	4	US-09-118-408-23 Sequence 23, Appl
25	56.4	3.3	3181	1	US-08-655-086-1 Sequence 1, Appl
26	55.8	3.3	1839	1	US-08-383-744-1 Sequence 1, Appl
27	55.8	3.3	1839	2	US-08-999-336-1 Sequence 1, Appl

28	55.8	3.3	1839	5	PCT-US96-01427-1	Sequence 1, Appl
29	55.6	3.2	4359	4	US-09-484-970B-4	Sequence 4, Appl
30	54.2	3.2	392	4	US-09-404-879A-372	Sequence 372, App
31	54.2	3.2	1333	4	US-09-227-357-51	Sequence 51, Appl
32	53.2	3.1	324	4	US-09-404-879A-290	Sequence 290, App
33	53	3.1	1416	2	US-07-621-091G-1	Sequence 1, Appl
34	53	3.1	1416	2	US-08-399-889-1	Sequence 1, Appl
35	53	3.1	1416	3	US-09-167-364-1	Sequence 1, Appl
36	53	3.1	1416	4	US-09-439-897-1	Sequence 1, Appl
37	51.8	3.0	2543	1	US-08-555-669-11	Sequence 11, Appl
38	51.8	3.0	2543	3	US-09-073-663-11	Sequence 11, Appl
39	51.2	3.0	38584	4	US-09-453-702B-50	Sequence 50, Appl
40	51	3.0	444	4	US-09-397-787-161	Sequence 161, App
41	50.6	3.0	4031	1	US-08-159-784-1	Sequence 1, Appl
42	50.2	2.9	9827	4	US-09-453-702B-66	Sequence 66, Appl
43	49.8	2.9	983	4	US-09-247-155-153	Sequence 153, App
44	49.2	2.9	1347	4	US-09-140-804-1	Sequence 1, Appl
45	48.8	2.9	1608	4	US-09-029-348-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1									
US-09-188-930-28									
Sequence 28, Application US/09188930A									
Patent No. 6150502									
GENERAL INFORMATION:									
APPLICANT: Watson, James D.									
APPLICANT: Strachan, Lorna									
APPLICANT: Sleeman, Matthew									
APPLICANT: Omrust, Rene									
APPLICANT: Morrison, James Greg									
TITLE OF INVENTION: Compositions Isolated From Skin Cells									
FILE OF INVENTION: and Methods For Their Use									
FILE REFERENCE: 11000.1011c1									
CURRENT APPLICATION NUMBER: US/09/188,930A									
CURRENT FILING DATE: 1998-11-09									
NUMBER OF SEQ ID NOS: 348									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO: 28									
LENGTH: 1123									
TYPE: DNA									
ORGANISM: Rat									
US-09-188-930-28									
Query Match									
Best Local Similarity 40.7%; Score 696.2; DB 3; Length 1123;									
Matches 819; Conservative 82.8%; Pred. No. 3e-195;									
Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2;									
OY	33	CTCTGCTGCTCTTCAAGGAGACTGTGAGGCTGTGTGAGAAATCATGCTTTGGAGCGC	92						
DB	136	CCCATGAGTCTCCCGGCGGAGATTGCGCATTTGTACAGGCATGCTCAGAGCGCAGC	195						
OY	93	TCATCTATGGAAGTCAAGTGGCTTTGTTTCCCTTTTGGCTGCTGTCAAGATGAT	152						
DB	196	TCCTCTGCTGAGCTGCTGCTGCTGCTTTTCTCCATTTTGGCTGTGCAAGATGAT	255						
OY	153	ACATGAGTCTCCCAACCGAGAGACTTACCCAGACTGAGTAAAGTGTTCATGAG	212						
DB	256	ACATGAGTCTCCCAACCGAGAGACTGAGTAAAGTGTTCATGAGTAAAGTGTTCATGAG	315						
OY	213	ACTACAGCTTTGAGGCTACCAAGGCCCCCTGGGCCACCGGCGCTCTGCGATTCCAG	272						
DB	316	ATATGAGTCTCCCTGCTTACCAAGGCCCCCTGGGCCACCGGCGCTCTGCGATTCCAG	375						
OY	273	GAAACCATGGAACCATGGAACCATGGAACCATGGAACCATGGAACCATGGAACCATGGA	332						
DB	376	GAAACCATGGAACCATGGAACCATGGAACCATGGAACCATGGAACCATGGAACCATGGA	435						
OY	333	AGGCGACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	392						
DB	436	AAGGACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	495						

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Oy 393 AGAGGGGCTACCCGGGAGTTCACACAGAACTTCAATTCAGATTCATTCGGCTCTCGGCA 452
Db 496 AGAAGGGATATCCAGGGGTGGCCACAGAGCTGCACATTTGGCTTCAATGGCTTCTTAGA 555
Oy 453 CCCACTTTCAGCAATCAGAAACAGTGGGATTTATCTTCAGCAGTGTGGAGACCAACATTGGAA 512
Db 556 CTCACCTTCAGCAATCAGAAACAGTGGCATTTATCTTCAGCAGTGTGGAGACCAACATTGGAA 615
Oy 513 ACTCTTTGATGTATGACTGTGATGATTTGGGGCCCCAGATCAGGTGTGATTTCTTCA 572
Db 616 ACTCTTTGATGTATGACTGTGATGATTTGGGGCCCCAGATCAGGTGTGATTTCTTCA 675
Oy 573 CCTTCAGCATGATGAAAGCATGAGATGTTTGGGAGAGTGTATGTACCTTTATGACCAATG 632
Db 676 CCTTCAGCATGATGAAAGCATGAGATGTTTGGGAGAGTGTATGTACCTTTATGACCAATG 735
Oy 633 GCACACAGCTCTTCAGCATGTACACCTATGAAATGAAAGGGCAAAATCAGATCATTCACAGA 692
Db 736 GTAACACGGTGTTCAGCATGTACACCTATGAAATGAAAGGGCAAAATCAGATCATTCACAGA 795
Oy 693 ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGCTTTGGCTGCCAATGGCG 752
Db 796 ACCATGACAGTGTGAAAGTGGCCAAAGGAGATGAAAGTGTGGCTAAGAAATGGGCAAGGTG 855
Oy 753 CTCCTCAGTGGGACACCAACAGCCTCTCACCTTTGGAGAGATTCCTGGCTTTGAAACTA 812
Db 856 CCTTCATGAGGGACCAACAGCCTCTCTACCTTTCGACAGGCTTTTGGCTTTTGAACCTA 915
Oy 813 AGTAATATATGACTAGAAATAGCTCAGCTTGGGGAGAACTGTAGCTGAGCT -GATTG 871
Db 916 AGTATGAGGAAGTACAGGATAGCTCCATGCTPAAAGGCGATTGTGAGTGAGCTAGGGTTG 975
Oy 872 TTACATCTGAGGAACATTAAGTTGAGGGTTTTCATTTGCTGTATTCAAAAATTAATTG 931
Db 976 TTAGATATCGAGGGGTGTTGGAGTTG -GGCTTCTCATGAGACTATTTAACCTTACATTG 1034
Oy 932 GTTGAATGTTGTACGCTACAGCTACAGCAACCAATATGTGGCAATTCAGGGGCTCAGA 991
Db 1035 GTACACACTGCTACTATTTCTAATGSCATACCAATTAATGTTGATCTTTAGGGGCTAGGA 1094
Oy 992 AGAATCAACCAACAAATAGTCTTCTCAGA 1020
Db 1095 AGAATAGACCAACAGTATATTTCCACAGA 1123

RESULT 2
US-09-188-930-203
; Sequence 203, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlson, James Greg
; TITLE OF INVENTION: Compositions and methods for their use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 1123
; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-203

```

OY	33	CTCGCGTGTCTCTCAGGGAGACTCTGAGAGCTGTGGTAATGATTCAGCTTTGGAGGACG	92
Db	136	CCCATCAGCTTCCCGGGGGAGATTCTGGCCGATTGTGCAGGACCATGCTCAGGAGGACGC	195
OY	93	TCATCTATTGGCAACCTGCTGGCTTTTCTTTTCTCCCTCTTTTGGCTGCTCAAGATGAT	152
Db	196	TGCGTCTGGTGGCACTGCTGCTGGCTTTCTCTTTTCTCCCATTTTGGCTGTGTCAAGATGAT	255
OY	153	ACATGAGTCTCCACANAACCGAGACTACCCCCAGACTGCAGTAACTGTTCATGGAG	212
Db	256	ACATGAGTCTCCACAGAGCTGAGGAGACTCCCCACAGACTGCAAGAGTGTTCATGGAG	315
OY	213	ACTGACACTTTCAGAGCTNCCAGAGCCCCCTGGGCTACACGGGGCCCTCTGGCATTTCCAG	272
Db	316	ATTATGTGATTCGGTGTGTACCAAGGGCCCCCTGGAGCCCCCAGAGTCTCTCTGGCATTTCCAG	375
OY	273	GAAACCATGTGAACAATGAGGCAATGAGAGCCACTGGTATCAAGAGAGCCAAAGTGTGAGA	332
Db	376	GAAACCATGTGAACAATGAGAAATACGAGAGCCACTGTCACAGAGGGGCGCAAGGTTGAGA	435
OY	333	AGGGCGCAAAAGGTGACTCTGGGGCCCTCGAGGGGAGCGGGGGGAGCATGGCCCCAAAGAG	392
Db	436	AAGGAGCAAAAGGAGCATCTGGGGCTCTCGAGGGGAACGGGGGAGCATGGCCCCAAAGAT	495
OY	393	AGAAAGGCTACCGGGGATTCACACAGAACTTCAGATTGCTCATTCAGTCTCTCGGCA	452
Db	496	AGAAAGGATATCCCGGGGCTCCACACAGAGCTGAGATTGCTTTCATGGCTTCTTCAGGCA	555
OY	453	CCCACTTCAGCAATCACAAGAGTGGGATTAATCTCGACAGTGTGAGAACCAATTGGAA	512
Db	556	CTCACTTCAGCAATCACAAGAGTGGGATTAATCTTCAGCAGTGTGAGAACCAATTGGAA	615
OY	513	ACTCTTTGATGTCTACTACTGCTGATGATTTTGGGGCCCCACCATATCAGAGTGTATTTCTTCA	572
Db	616	ACTCTTCGATGTCTACTACTGATGATTTTGGGGCCCCGATACAGGCGTATTTCTTCA	675
OY	573	CTCTTACAGTGAAGCATGAGAGTGTGGAGAGTGTATGTGTACCTTATGACAAATG	632
Db	676	CTCTTACAGTGAATGAACATGAGAGTGTGGAGAGTGTATGTGTACCTTATGACAAATG	735
OY	633	GCAACACAGTCTTACGATTCAGCTATGAGTATGAATGAAGGGCAATACGATACATCCAGCA	692
Db	736	GTAACACGGTGTTCAGATCTACACTATGAACAAAGGGAAATCAGATACATCCAGCA	795
OY	693	ATCATCTGCTGCTGACACTGACCCAAAGGGGATGAGTGTGGCTGGGAATGGGCAATGGCG	752
Db	796	ACCATGCACTGCTCAABATTTGGGCCAAAGAGATCAACTGTGCTTAGAAGATGGGCAACGGTG	855
OY	753	CTCTCCATGGGGACCAACAAGCTTCTCCACCTTTTGCAGATTTCTGTCTTTGAACCTA	812
Db	856	CCCTCCATGGGGACCAACAAGCTTCTCTACCTTCTCCAGAGCTTCTGTCTTTTGAACCTA	915
OY	813	AGTAATATATGACTAATAATAGCTCCACTTTGGGGAAAGCTGTAGCGAGCT -GATTTG	871
Db	916	AGTATGTGGAAGTCAAGATAATGCTCATAGCTAAGGGCGCATTTGTAGTGAAGCTAGAGTTG	975
OY	872	TTAGCATGTGGAACAATTAAAGTTGAGGGTTTATCATGTGCTGTATCAAAAATTAATTATG	931
Db	976	TTAGCATGTGAGGGGTTTGGAGTTG -GGCTTCTCATGTAGAGATTTTAACTGTTACATTTG	1033
OY	932	GTTGCAATGTTTTCACGCTACAGGTAACACCAATAATGTTGGACAAATTCAGGGGCTCAGA	991
Db	1035	GTCACACTGCTACTCATTTATATGGCATACCAATTAATGTTGATTACTTTAGGGGCTTAGGA	1094
OY	992	AGATCAACCAACAAATAGTCTTCTCAGA 1020	
Db	1095	AGATATAGCCACAAGATTAATTTCCCGAA 1123	

Query Match	4.6%	Score 78.8	DB 4	Length 3275
Best Local Similarity	52.4%	Pred. No. 5.2e-13		
Matches 173; Conservative	0	Mismatches 157	Indels 0	Gaps 0

RESULT 4
US-08-463-911-6

1 APPLICANT: Scherer, Philipp E.
2 APPLICANT: Lodish, Harvey F.
3 TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
4 TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
5 NUMBER OF SEQUENCES: 7
6 CORRESPONDENCE ADDRESS:
7 ADDRESS: Hamilton, Brook, Smith & Reynolds, P.
8 STREET: Two Militia Drive
9 CITY: Lexington
10 STATE: Massachusetts
11 COUNTRY: USA
12
13 ZIP: 02173
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent Release #1.0, Version #1.30
20 CURRENT APPLICATION NUMBER: US/08/463,911
21
22 APPLICATION NUMBER: US/08/463,911

Query Match	4.4%	Score 74.6	DB 2	Length 1313
Best Local Similarity	50.4%	Pred. No. 5.4e-12		
Matches 210	Conservative 0	Mismatches 204	Indels 3	Gaps 1

[illegible]

```

RESULT 5
US-09-140-804-9
; Sequence 9, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 4517
; TYPE: DNA
; ORGANISM: Homo sapiens

```


DR N-PSDB: AAA95787.
 XX New human immune system molecules 1-15 and polynucleotides encoding
 PT them useful for diagnosing, treating or preventing e.g. immunological
 PT disorders, infections, cell proliferative disorders, microbial
 PT infections
 XX
 XX Claim 1: Page 85; 95pp; English.

XX This sequence represents a human immune system molecule (IMOL) encoded
 CC by the cDNA isolated as clone 1890540 from the Incyte BLA0707 library.
 CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides
 CC (AAA95775-95789), and compositions comprising them are useful for the
 CC diagnosis, treatment or prevention of immunological disorders,
 CC infections and cell proliferative disorders, including cancer. The IMOL
 CC may be used to treat or prevent disorders associated with decreased
 CC expression or activity of IMOL, such as immunological disorders
 CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),
 CC hematopoietic cancer, infections caused by virus (e.g. adenovirus,
 CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,
 CC Shigella), fungi (e.g. Aspergillus, Blastomycetes), parasites (e.g.
 CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative
 CC disorders (e.g. actinic keratosis, arteriosclerosis, psoriasis), and
 CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also
 CC useful as immunogens for the development of antibodies that
 CC specifically recognizes these peptides. The polynucleotides may be used
 CC to detect and quantify gene expression in biopsied tissues in which
 CC expression of IMOL may be correlated with the disease, as targets in a
 CC microarray, to detect differences in gene sequences among normal,
 CC carrier and affected individuals, and for screening libraries of
 CC compounds in drug screening techniques. Antibodies which specifically
 CC bind to IMOL may be used for the diagnosis of disorders characterized
 CC by expression of IMOL, or in assays to monitor patients being treated
 CC with IMOL or agonists, antagonists, or inhibitors of IMOL.
 CC
 XX Sequence 246 AA:

SO Query Match 100.0%; Score 1367; DB 21: Length 246;
 Best Local Similarity 100.0%; Pred. No. 2e-124;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWRQLYVWLLALFLPCLCODEYMESPQTGGLPPDCKCHGDSFPGYGPPEPPG 60
 DB 1 MLWRQLYVWLLALFLPCLCODEYMESPQTGGLPPDCKCHGDSFPGYGPPEPPG 60
 QY PCGIPGNHGNNGNNGATGHEGAKGEGKDGKDLPRGREGOHGKGEKGYGIPPELOIAF 120
 DB 61 PCGIPGNHGNNGNNGATGHEGAKGEGKDGKDLPRGREGOHGKGEKGYGIPPELOIAF 120
 QY 121 MASLATHFSNONGIIFSSVETNIGNEFDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV 180
 DB 121 MASLATHFSNONGIIFSSVETNIGNEFDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV 180
 QY 181 YLMHNGNTVFSMTSEYEMKKSOTSSNHAVALKLAKGDEVLMRMNGALHGHORSTFAGF 240
 DB 181 YLMHNGNTVFSMTSEYEMKKSOTSSNHAVALKLAKGDEVLMRMNGALHGHORSTFAGF 240
 QY 241 LLEFETK 246
 DB 241 LLEFETK 246

RESULT 2
 AAB29580
 ID AAB29580 standard; Protein: 246 AA.
 XX
 AC AAB29580;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Human adipocyte complement related protein homologue zacr3, SEQ ID NO.2.
 XX
 KW Human zacr3; adipocyte complement related protein homologue;

KW ACR30; C1q domain; collagen-like domain; energy balance modulation;
 KW cellular metabolism; metabolic disorder; obesity; anorexia;
 KW antimicrobial agent; infection; platelet aggregation inhibition;
 KW adhesion; activation; vascular injury; antibacterial; antiviral.
 XX
 OS Homo sapiens.
 XX
 PN WO200063377-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 19-APR-2000; 2000WO-US10454.
 XX
 PR 20-APR-1999; 9905-0294943.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Piddington CS, Bishop PD;
 XX
 DR WPI: 2000-665243/64.
 DR N-PSDB: AAC64058.

XX Novel zacr3 polypeptides used to treat or prevent bacterial or viral
 PT infections, for wound healing, improving blood flow, and to analyze
 PT energy efficiency in mammals.
 XX
 PS Claim 2: Page 109-110; 123pp; English.

XX The invention relates to the human zacr3 protein (AAB29580) and to
 CC nucleic acids which encode it (AAC64058, AAC64053). Zacr3 is a homologue
 CC of adipocyte complement related protein (ACRP30) and contains
 CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
 CC C-terminal C1q domain comprising 10 beta-strands. The zacr3 gene is
 CC located on chromosome 5p12. The invention also relates to zacr3
 CC fragments, fusion proteins containing zacr3 polypeptides,
 CC zacr3-specific antibodies, expression constructs and host cells
 CC comprising zacr3 nucleic acids, and methods of recombinant production of
 CC zacr3. Human zacr3, and its agonists and antagonists may be used in the
 CC study and modulation of cellular metabolism and energy balance in
 CC mammals, and may therefore be used to treat disorders such as obesity and
 CC anorexia, and conditions associated with these disorders. Due to its C1q
 CC like domain, zacr3 and zacr3-containing fusion proteins may be useful
 CC as antimicrobial agents, promoting lysis or phagocytosis of infections
 CC organisms such as bacteria or viruses. Zacr3, its fragments, fusion
 CC proteins, antibodies and activity modulators may also be used to inhibit
 CC collagen-induced platelet aggregation, adhesion, or activation, and may
 CC therefore have potential for promoting blood flow within the vasculature
 CC of a mammal e.g., to treat injury to the vasculature or other collagenous
 CC tissue. Human zacr3 and its antibodies may additionally be used to study
 CC dimerisation and oligomerisation. The present sequence represents human
 CC zacr3.
 CC
 XX

SO Sequence 246 AA:
 Query Match 100.0%; Score 1367; DB 21: Length 246;
 Best Local Similarity 100.0%; Pred. No. 2e-124;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLWRQLYVWLLALFLPCLCODEYMESPQTGGLPPDCKCHGDSFPGYGPPEPPG 60
 DB 1 MLWRQLYVWLLALFLPCLCODEYMESPQTGGLPPDCKCHGDSFPGYGPPEPPG 60
 QY PCGIPGNHGNNGNNGATGHEGAKGEGKDGKDLPRGREGOHGKGEKGYGIPPELOIAF 120
 DB 61 PCGIPGNHGNNGNNGATGHEGAKGEGKDGKDLPRGREGOHGKGEKGYGIPPELOIAF 120
 QY 121 MASLATHFSNONGIIFSSVETNIGNEFDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV 180
 DB 121 MASLATHFSNONGIIFSSVETNIGNEFDVMTGRFGAPVSGVYFFTFSSMKHEDVEEYV 180
 QY 181 YLMHNGNTVFSMTSEYEMKKSOTSSNHAVALKLAKGDEVLMRMNGALHGHORSTFAGF 240
 DB 181 YLMHNGNTVFSMTSEYEMKKSOTSSNHAVALKLAKGDEVLMRMNGALHGHORSTFAGF 240

XX AAB8447;
 AC
 DT 23-MAY-2001 (first entry)
 DE Human membrane or secretory protein clone PSEC0232.
 XX
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;
 XX rheumatoid arthritis; diabetes.
 OS Homo sapiens.
 XX
 PN EPI067182-A2.
 XX
 PD 10-JAN-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114090.
 XX
 PR 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 XX
 DR MPI: 2001-093989/11.
 DR N-PSDB: AAF93874.
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 XX
 PS Claim 1: SEQ ID 262: 609pp + CD ROM; English.
 XX
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to
 CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid
 CC arthritis and diabetes.
 CC
 XX
 SQ Sequence 246 AA;
 Query Match 100.0%; Score 1367; DB 22; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2e-124;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIMRLIYQQLALFLFPCQLQDEYMSPTQGLPPDCSKCHSDYSGRGYQGPFG 60
 DB 1 MIMRLIYQQLALFLFPCQLQDEYMSPTQGLPPDCSKCHSDYSGRGYQGPFG 60
 QY 61 PPGIGNNGNNGNNGCATGHEGAKGKGKDGKDLGPRGGRGQHHPKGEKGYGPIPELQIAF 120
 DB 61 PPGIGNNGNNGNNGCATGHEGAKGKGKDGKDLGPRGGRGQHHPKGEKGYGPIPELQIAF 120

QY 121 MASLATHFSNONGIIFSSVETNIGNPFDMVMTGRGAPVSGVYFFTFSSMKHEDVEEYV 180
 DB 121 MASLATHFSNONGIIFSSVETNIGNPFDMVMTGRGAPVSGVYFFTFSSMKHEDVEEYV 180
 QY 181 YLMHNGNTVFSYSEYEMKKSQDTSNHAVALKLAKDEYWLRMGNCALHGDHQFSTFAGF 240
 DB 181 YLMHNGNTVFSYSEYEMKKSQDTSNHAVALKLAKDEYWLRMGNCALHGDHQFSTFAGF 240
 QY 241 LLEFRK 246
 DB 241 LLEFRK 246

RESULT 5

ID AA084371 standard; Protein: 246 AA.

AC AA084371;

DT 08-MAY-2002 (first entry)

DE Novel human secreted or membrane-associated protein #10.

KW Human; secreted protein; membrane-associated protein; hypertension;
 KW inflammatory disorder; neurological disorder; haematopoietic disorder;
 KW skeletal developmental disorder; growth abnormality; autoimmune disorder;
 KW neurodegenerative disorder; nervous system disorder; bacterial infection;
 KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
 KW hypotension; sexual development disorder; blood disorder.

XX Homo sapiens.

OS WO200204600-A2.

PN 17-JAN-2002.

PF 12-JUL-2001; 2001WO-US21985.

PR 12-JUN-2000; 2000US-218033P.

PR 21-AUG-2000; 2000US-226517P.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PA (GLAX) GLAXO GROUP LTD.

PI Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
 PI Smith R, Xiang Z, Xie Q;
 DR MPI: 2002-188468/24.
 DR N-PSDB: ABK35591.

PT Novel secreted and membrane-associated polypeptides and polynucleotides
 PT encoding the polypeptides, for preventing, treating and ameliorating
 PT cancers, mental or sexual developmental disorders, and malignant tumours

PT Claim 1: Page 131-132; 151pp; English.

XX The present invention relates to the isolation of novel human secreted
 XX or membrane-associated proteins and the genes encoding them. The
 XX sequences of the invention are useful for treating, preventing and
 XX ameliorating various diseases such as inflammatory disorders (e.g.
 XX asthma), neurological disorders (e.g. dementia), haematopoietic
 XX disorders, skeletal developmental disorders, growth abnormalities,
 XX neurodegenerative disorders (e.g. Huntington's disease), nervous system
 XX disorders, autoimmune disorders (e.g. rheumatoid arthritis),
 XX peripheral myelinopathies, viral and bacterial infections,
 XX alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
 XX hypotension, obesity, bulimia, anorexia, manic depression, delirium,
 XX mental retardation, Tourette's syndrome, schizophrenia, growth, mental
 XX or sexual development disorders, and dysfunctions of the blood cascade
 XX system including those leading to stroke. AA084362-AA084389 represent
 CC the novel human secreted or membrane-associated proteins of the

CC invention.
XX
SQ Sequence 246 AA:
Query Match 100.0%; Score 1367; DB 23; Length 246;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLMRLIYWOLLAFLFPLFCCLCODEYMEPOTGGLPPCCKCHGDSFRRGQGPFG 60
Db 1 MLMRLIYWOLLAFLFPLFCCLCODEYMEPOTGGLPPCCKCHGDSFRRGQGPFG 60
QY 61 PPGIIPNHNNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEKGYPGIPELQIAF 120
Db 61 PPGIIPNHNNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEKGYPGIPELQIAF 120
QY 121 MASLATHFSNONGIIFSSVEFNIGNFEDVMTGRGAPVSGYFFTFSMKHEDVEEYV 180
Db 121 MASLATHFSNONGIIFSSVEFNIGNFEDVMTGRGAPVSGYFFTFSMKHEDVEEYV 180
QY 181 YLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMNGALHGDHQRSTFAGF 240
Db 181 YLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMNGALHGDHQRSTFAGF 240
QY 241 LLEFETK 246
Db 241 LLEFETK 246
RESULT 6
ID AA084370 standard; Protein: 319 AA.
AC AA084370;
XX 08-MAY-2002 (first entry)
XX Novel human secreted or membrane-associated protein #9.
XX Human: secreted protein: membrane-associated protein: hypertension;
KW inflammatory disorder; neurological disorder; haematopoietic disorder;
KW skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW neurodegenerative disorder; nervous system disorder; bacterial infection;
KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW hypotension; sexual development disorder; blood disorder.
XX Homo sapiens.
OS
XX WO200204600-A2.
XX 17-JAN-2002.
XX 12-JUL-2001; 2001WO-US21985.
XX 12-JUL-2000; 2000US-218033P.
XX 21-AUG-2000; 2000US-226517P.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX (GLAX) GLAXO GROUP LTD.
XX Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
XX Smith RF, Xiang Z, Xie O;
XX WPI: 2002-188468/24.
XX N-PSDB: ABR35390.
XX Novel secreted and membrane-associated polypeptides and polynucleotides
XX encoding the polypeptides, for preventing, treating and ameliorating
XX cancers, mental or sexual developmental disorders, and malignant tumours
PS Claim 1; Page 130-131; 151pp; English.

XX The present invention relates to the isolation of novel human secreted
CC or membrane-associated proteins and the genes encoding them. The
CC sequences of the invention are useful for treating, preventing and
CC ameliorating various diseases such as inflammatory disorders (e.g.
CC asthma), neurological disorders (e.g. dementia), haematopoietic
CC disorders, skeletal developmental disorders, growth abnormalities,
CC neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC peripheral myelinopathies, viral and bacterial infections,
CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC mental retardation, Tourette's syndrome, schizophrenia, growth, cascade
CC or sexual development disorders, and dysfunctions of the blood cascade
CC system including those leading to stroke. AA084372-AA084389 represent
CC the novel human secreted or membrane-associated proteins of the
CC invention.
XX
SQ Sequence 319 AA;
Query Match 96.6%; Score 1320.5; DB 23; Length 319;
Best Local Similarity 77.1%; Pred. No. 9.3e-120;
Matches 246; Conservative 0; Mismatches 0; Indels 73; Gaps 1;
QY 1 MLMRLIYWOLLAFLFPLFCCLCODEYME-----SPOTGGLPPCCKCHG 28
Db 1 MLMRLIYWOLLAFLFPLFCCLCODEYME-SGRTNKVARIYOSHQGRSGSRREKVER 60
QY 29 -----
Db 61 SHPKTGYDNNSTDLKLRLDELPHPREVDDLAQITTTWGSPOFGGLPPCCKCHG 120
QY 48 SFRGYGPPGPPGPPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEK 107
Db 121 SFRGYGPPGPPGPPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKEK 180
QY 108 GYPIPELQIAFMAASLATHFSNONGIIFSSVEFNIGNFEDVMTGRGAPVSGYFFTF 167
Db 181 GYPIPELQIAFMAASLATHFSNONGIIFSSVEFNIGNFEDVMTGRGAPVSGYFFTF 240
QY 168 SMKHEDVEEYVYLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMNGAL 227
Db 241 SMKHEDVEEYVYLMHNGNTVFSYSEMKGKSDTSSNHAVALKLAKGDEVLMRMNGAL 300
QY 228 HGDHQRSTFAGFLLETK 246
Db 301 HGDHQRSTFAGFLLETK 319
RESULT 7
ID AAB29582 standard; Protein: 246 AA.
AC AAB29582;
XX 19-FEB-2001 (first entry)
XX Mouse zacr2 protein, SEQ ID NO:12.
XX Mouse zacr2 protein, SEQ ID NO:12.
XX Mouse zacr2; adipocyte complement related protein homologue;
KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW cellular metabolism; metabolic disorder; obesity; anorexia;
KW antimicrobial agent; infection; platelet aggregation inhibition;
KW adhesion; activation; vascular injury; antibacterial; antiviral;
KW human zacr3 homologue.
XX Mus musculus.
OS
XX WO2000063377-A1.
XX 26-OCT-2000.
XX 19-APR-2000; 2000WO-US10454.
PF

XX 20-APR-1999; 99US-0294943.
XX (ZYMO) ZYMOGENETICS INC.
XX Piddington CS, Bishop PD;
XX MPI: 2000-665243/64.
XX N-PSDB: AAC64064.
XX
XX Novel zacr3 polypeptides used to treat or prevent bacterial or viral
XX infections, for wound healing, improving blood flow, and to analyze
XX energy efficiency in mammals -
XX
XX Disclosure; Page 117-118; 123pp; English.
XX
XX The invention relates to the human zacr3 protein (AAB29580) and to
XX nucleic acids which encode it (AAC64058, AAC64063). Zacr3 is a homologue
XX of adipocyte complement related protein (ACRP30) and contains a
XX collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a
XX C-terminal C1q domain comprising 10 beta-strands. The zacr3 gene is
XX located on chromosome 5p12. The invention also relates to zacr3
XX fragments, fusion proteins containing zacr3 polypeptides,
XX zacr3-specific antibodies, expression constructs and host cells
XX comprising zacr3 nucleic acids, and methods of recombinant production of
XX zacr3. Human zacr3, and its agonists and antagonists may be used in the
XX study and modulation of cellular metabolism and energy balance in
XX mammals, and may therefore be used to treat disorders such as obesity and
XX anorexia, and conditions associated with these disorders. Due to its C1q
XX like domain, zacr3 and zacr3-containing fusion proteins may be useful
XX as antimicrobial agents, promoting lysis or phagocytosis of infectious
XX organisms such as bacteria or viruses. Zacr3, its fragments, fusion
XX proteins, antibodies and activity modulators may also be used to inhibit
XX collagen-induced platelet aggregation, adhesion, or activation, and may
XX therefore have potential for promoting blood flow within the vasculature
XX of a mammal e.g., to treat injury to the vasculature or other collagenous
XX tissue. Human zacr3 and its antibodies may additionally be used to study
XX dimerisation and oligomerisation. The present sequence represents mouse
XX zacr3, a homologue of human zacr3.
XX
XX
SO Sequence 246 AA;
Query Match 95.9%; Score 1311; DB 21; Length 246;
Best Local Similarity 95.9%; Pred. No. 5.5e-119;
Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 MIMQILYMWLLAFPLPFCICDEYHESPTGGLPPDCSCCHGDSFRGYCPGPPG 60
DB 1 MGRQRIMWHLLPLFLPFCICDEYHESPPAGGLPPDCSCCHGDSFRGYCPGPPG 60
QY 61 PPGIPGHHNGNNGANGHGEKAGEKDGKDLGPRGEGCHGPRGEGKGYRPIPELQIAF 120
DB 61 PPGIPGHHNGNNGANGHGEKAGEKDGKDLGPRGEGCHGPRGEGKGYRPIPELQIAF 120
QY 121 MASLATHFSNONSIIITSSVETNIGNEFDVMTGRFGAPVSGVYFTFSMKHEDVEEYV 180
DB 121 MASLATHFSNONSIIITSSVETNIGNEFDVMTGRFGAPVSGVYFTFSMKHEDVEEYV 180
QY 181 YLMHNGTVESMYSYEMKGSQDSSNHAVALKLAKGDEVYLMRGALGHQRETFEAGF 240
DB 181 YLMHNGTVESMYSYEMKGSQDSSNHAVALKLAKGDEVYLMRGALGHQRETFEAGF 240
QY 241 LLEFETK 246
DB 241 LLEFETK 246
RESULT 8
ID AAM99925 standard; Protein: 225 AA.
XX AAM99925;
XX

DT 07-JAN-2002 (first entry)
XX
XX Human polypeptide SEQ ID NO 41.
DE
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX anti-allergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.
XX
XX Homo sapiens.
XX
XX MO20015173-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001MO-US01356.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216647.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217487.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.

```
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 26-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.

XX
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451924/48.
XX DR N-PSDB; AA199523.
XX
XX PT New nucleic acids and polypeptides, useful for treating, preventing or
XX ameliorating human disorders and diseases -
XX
XX PS Claim 11; SEQ ID NO 41; 465pp + Sequence Listing; English.
XX
XX CC The invention relates to novel human polynucleotides (AA199513-AA199518)
XX and the encoded proteins (AA199515-AA199534) which are useful for
XX preventing, treating or ameliorating medical conditions e.g. by protein
XX or gene therapy. The genes are isolated from a range of human tissues
XX disclosed in the specification. The nucleic acids, proteins, antibodies
XX and (ant)agonists are useful in the diagnosis, treatment and prevention
XX of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
XX adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
XX lung, or urogenital; (b) immune disorders e.g. Addison's disease,
XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
XX arthritis and ulcerative colitis; (c) cardiovascular disorders such as
XX myocardial ischaemias; (d) wound healing; (e) neurological diseases
XX e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as
XX viral, bacterial, fungal and parasitic infections.
XX CC Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX SQ Sequence 225 AA:

Query Match 88.4%; Score 1208; DB 22; Length 225;
Best Local Similarity 99.5%; Pred. No. 4.9e-109;
Matches 218; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 28 ESPQTGGLPPDCSKCHDYSFRGYGPPGPPGPGIGTGNHNNNGNATGHEGAKGKG 87
DB 7 OSPTGGLPPDCSKCHDYSFRGYGPPGPPGPGIPGNHNNNGNATGHEGAKGKG 66
QY 88 DKGDGPPRGGRGHPGPKGEGKGPPIPELQIFMASLATHFNSNGSIIFFSVETNIGNF 147
DB 67 DKGDGPPRGGRGHPGPKGEGKGPPIPELQIFMASLATHFNSNGSIIFFSVETNIGNF 126
QY 148 FDVMTGREGAPYGVYFFTFSSMKHEDVEEYVYLMHNGNTVFSMYSEMKGSDTSSNH 207
DB 127 FDVMTGREGAPYGVYFFTFSSMKHEDVEEYVYLMHNGNTVFSMYSEMKGSDTSSNH 186
QY 208 AVLKLAGDEVLBMGNGALHGDHOFSTFAGFLPETK 246
DB 187 AVLKLAGDEVLBMGNGALHGDHOFSTFAGFLPETK 225

RESULT 9
AA1860
ID AA1860 standard; Protein; 202 AA.
XX
XX AC AA1860;
XX
XX DT 22-OCT-2001 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 6791.
XX
```

KW Human: nootropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 OS Homo sapiens.
 XX
 XX MO200153312-A1.
 XX
 XX
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000MO-US34263.
 XX
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Dirmanac RT;
 XX
 XX WPI: 2001-442253/47.
 DR N-PSDB; AAI61016.

PT Novel nucleic acids and polypeptides, useful for treating disorders
 XX such as central nervous system injuries -
 XX
 XX Example 2: SEQ ID NO 6791; 10078pp: English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA158642-AA162213) with nootropic,
 CC immunosuppressant and cytosolic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 202 AA:

Query Match 64.7%; Score 884; DB 22; Length 202;
 Best Local Similarity 84.2%; Pred. No. 1.2e-77;
 Matches 170; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 77 TTEHGAAGKGGKGGDGGPRGGGQHPRKGGKGGPGGPP----- 115
 DB 1 TTEHGAAGKGGKGGDGGPRGGGQHPRKGGKGGPGGPP----- 60
 QY 116 -----LQIAFMASLATHFSNONGIIFSSVETNIGNFEFDMTGRFGAPVSGYF 164
 DB 61 ILTPDLEKIGQIAFMASLATHFSNONGIIFSSVETNIGNFEFDMTGRFGAPVSGYF 120
 QY 165 FTFSMKHEDEVEVYVYLMHNGNTVFSMTSYEMKCKSDSSNMHAYLKLAKGDEWLMRGN 224
 DB 121 FTFSMKHEDEVEVYVYLMHNGNTVFSMTSYEMKCKSDSSNMHAYLKLAKGDEWLMRGN 180

QY 225 GALGHQHPSTFAGFLFETK 246
 DB 181 GALGHQHPSTFAGFLFETK 202

RESULT 10

AAE06589
 ID AAE06589 standard; Protein; 223 AA.

XX AAE06589;

DT 25-SEP-2001 (first entry)

DE Human protein having hydrophobic domain, HP10781.

XX Human: hydrophobic domain; gene therapy; nutritional supplement;
 KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytosolic;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; antifertility; antiinflammatory.
 XX

OS Homo sapiens.

PN MO200149728-A2.

PD 12-JUL-2001.

PF 28-DEC-2000; 2000MO-JP09359.

PR 06-JAN-2000; 2000JP-0000585.

PR 06-JAN-2000; 2000JP-0000588.

PR 11-JAN-2000; 2000JP-0002299.

PR 03-FEB-2000; 2000JP-0026862.

PR 03-MAR-2000; 2000JP-0058367.

XX (PROT-) PROTEGENE INC.

PA (SAGA) SAGAMI CHEM RES CENT.

XX Kato S, Kimura T;

DR WPI: 2001-418355/44.

XX N-PSDB: AAD12584.

PT Human proteins with hydrophobic domains and the nucleic acids encoding

PT them, useful for preventing diagnosing and treating e.g. cancer,

XX Alzheimer's and inflammation -

PS Claim 1: Page 308-309; 563pp: English.

XX The present sequence is human protein with hydrophobic domain,
 CC HP10781. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotides and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional
 CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate activin and inhibin activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 15, 2003, 19:35:56 ; Search time 36 Seconds
(without alignments)
201.057 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MLMROLIYQMLALFLPFC.....LHGDRHFRSTPAGFLFETK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUTS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	582	42.6	105	4	US-09-188-930-147
2	582	42.6	105	4	US-09-188-930-280
3	316	21.1	294	4	US-09-188-930-294
4	294	21.5	247	2	US-08-463-911-2
5	293.5	21.5	231	4	US-09-530-423-2
6	293.5	21.5	244	2	US-08-463-911-7
7	293.5	21.5	244	4	US-09-140-804-3
8	293.5	21.5	244	4	US-09-336-536-20
9	293.5	21.5	244	4	US-09-530-423-1
10	287	21.0	247	4	US-09-140-804-8
11	287	21.0	247	4	US-09-118-408-3
12	287	21.0	247	4	US-09-506-855-3
13	274	20.0	246	2	US-08-463-911-4
14	273	20.0	746	4	US-09-370-838-185
15	264.5	19.3	228	4	US-09-336-536-4
16	264.5	19.3	243	4	US-09-140-804-2
17	264.5	19.3	243	4	US-09-336-536-3
18	254.5	18.6	243	4	US-09-336-536-10
19	252.5	18.5	228	4	US-09-336-536-11
20	252.5	18.5	243	4	US-09-188-930-295
21	237.5	17.4	281	4	US-09-118-408-44
22	237.5	17.4	281	4	US-09-506-855-44
23	226	16.5	281	4	US-09-118-408-2
24	226	16.5	281	4	US-09-506-855-2
25	226	16.5	423	1	US-08-383-744-2
26	226	16.5	423	1	US-08-999-336-2
27	226	16.5	423	5	PCT-US96-01427-2

28	219	16.0	245	4	US-09-140-804-4	Sequence 4, Appl
29	202	14.8	215	4	US-09-140-804-5	Sequence 5, Appl
30	200.5	14.7	198	4	US-09-188-930-138	Sequence 138, App
31	196	14.3	222	4	US-09-140-804-7	Sequence 7, Appl
32	194	14.2	185	2	US-08-463-911-3	Sequence 3, Appl
33	192	14.0	623	4	US-09-029-348-3	Sequence 3, Appl
34	192	14.0	626	4	US-09-029-348-2	Sequence 2, Appl
35	186	13.6	236	4	US-09-140-804-6	Sequence 6, Appl
36	185	13.5	357	1	US-07-609-716-66	Sequence 66, Appl
37	185	13.5	357	1	US-08-642-255-33	Sequence 33, Appl
38	185	13.5	357	4	US-08-475-411A-66	Sequence 66, Appl
39	185	13.5	357	4	US-08-478-028A-66	Sequence 66, Appl
40	184.5	13.5	684	1	US-08-555-663-12	Sequence 12, Appl
41	184.5	13.5	684	3	US-09-073-663-12	Sequence 9, Appl
42	183.5	13.4	532	1	US-08-494-168-9	Sequence 7, Appl
43	183	13.4	489	2	US-08-794-795-7	Sequence 7, Appl
44	183	13.4	489	1	US-09-249-200-7	Sequence 2, Appl
45	183	13.4	518	1	US-08-392-367B-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-188-930-147
; Sequence 147, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 147
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-147

Query Match          42.6%; Score 582; DB 4; Length 105;
Best Local Similarity 93.3%; Pred. No. 2.1e-51;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLMROLIYQMLALFLPFCIDDEYVESPTQGLPPDCSKCGHDYSPFGYGGPPGPG 60
   |||:::|||||
DB 1 MLMROLIYQMLALFLPFCIDDEYVESPTQGLPPDCSKCGHDYSPFGYGGPPGPG 60
   |||:::|||||

QY 61 PPGIPGNHNNNGATGHEGAKGKGDGLPGRGGRGHPGK 105
   PPGIPGNHNNNGATGHEGAKGKGDGLPGRGGRGHPGK 105
DB 61 PPGIPGNHNNNGATGHEGAKGKGDGLPGRGGRGHPGK 105
   PPGIPGNHNNNGATGHEGAKGKGDGLPGRGGRGHPGK 105

RESULT 2
US-09-188-930-280
; Sequence 280, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
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;; CURRENT FILING DATE: 1998-11-09
;; NUMBER OF SEQ ID NOS: 348
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 280
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Rat
US-09-188-930-280

Query Match 42.6%; Score 582; DB 4; Length 105;
Best Local Similarity 93.3%; Pred. No. 2,1e-51;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MIMROLIYMOIALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGGPPPG 60
DB 1 MIMROLIYMOIALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGGPPPG 60
QY 61 PPGIGNHGNNNGNNGATGHEGAKGEGKDGKDLGPRGERGQHGPKG 105
DB 61 PPGIGNHGNNNGNNGATGHEGAKGEGKDGKDLGPRGERGQHGPKG 105

RESULT 3
US-09-188-930-294
; Sequence 294, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000,1011c1
; CURRENT APPLICATION NUMBER: US/09/188, 930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 294
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-294

Query Match 23.1%; Score 316; DB 4; Length 294;
Best Local Similarity 28.9%; Pred. No. 5,7e-24;
Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;

QY 6 LIYMOIALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGGPPPG 59
DB 10 MIMROLIYMOIALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGGPPPG 59
QY 60 PPGIGNHGNNNGNNGATGHEGAKGEGKDGKDLGPRGERGQHGPKG 105
DB 55 GPPGAPGSSGAWGRGFRGKDGQDGDGDEGEPGRTGNRGKQPGKAGALGA 114
QY 93 GPRGERGQHGPKGEGKDGKDLGPRGERGQHGPKGEGKDGKDLGPRGERGQHGPKG 105
DB 115 GPRGERGQHGPKGEGKDGKDLGPRGERGQHGPKGEGKDGKDLGPRGERGQHGPKG 105
QY 134 GIIFSSVETNIGNFFEDVMTGRGAPVSGVFFFTFSMM---KHEVEEYVYVLMNNGNVE 190
DB 175 PIKFDKILMNGGHHYMASSGKFFVCSVFOITFTDITLANKH---LAICLVHNGO--Y 227
QY 191 SMYSYEMK-GKSDTSSNHAIVLAKAGDEWLMR---GNGALHGDHOFSTFAGFLF 243
DB 228 RIRFEDANTGNHVDVASSGTLILAKKEGDEWMLQIFYSSEQNGLFIYPPYWDLSLFTGLIY 285

RESULT 4
US-08-463-911-2
; Sequence 2, Application US/08463911

;; Patent No. 5869310
;; GENERAL INFORMATION:
;; APPLICANT: Scherer, Philipp E.
;; APPLICANT: Lodish, Harvey F.
;; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
;; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
;; NUMBER OF SEQUENCES: 7
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/463,911
;; FILING DATE:
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 247 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-463-911-2

Query Match 21.5%; Score 294; DB 2; Length 247;
Best Local Similarity 31.5%; Pred. No. 7,4e-22;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

QY 6 LIYMOIALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGGPPPG 63
DB 2 LIYMOIALFLPFCICLDEYMEPOTGGLPPDCSKCHGDYSPFGYGGPPPG 63
QY 64 IPGNHGNNNGNNGATGHEGAKGEGKDGKDLGPRGERGQHGPKGEGKDGKDLGPRGERGQHGPKG 115
DB 49 HPNGHGTGPRGDRGDTPEKEGKDGKDLGPRGERGQHGPKGEGKDGKDLGPRGERGQHGPKG 108
QY 116 ---LQIAFMASLATHESNONGIIESSVETNIGNFFEDVMTGRGAPVSGVFFFTFSMM 170
DB 109 EAAVYMRSAFSGLETRVTPNVPRIFFKIFRYNOONHVDGSGKGYFCMIPGLIYFSYHT 168
QY 171 KHEVEEYVYVLMNNGNVEFMSYEMKGSNTSSNHAIVLAKAGDEWLMR---GNG 226
DB 169 VY---WKDVVSLFKKKAVALFTYDQYOKNVDASGVLLHLEVDQWMLQYVGGDHNG 226
QY 227 LAGDHOFSTFAGFLF 243
DB 227 LYADNVNDSTFTGLIY 243

RESULT 5
US-09-530-423-2
; Sequence 2, Application US/09530423
; Patent No. 6461821
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
; FILE REFERENCE: P98-51


```

CURRENT APPLICATION NUMBER: US/09/530.423
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: JP H9-297569
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 231
TYPE: PRT
ORGANISM: Abdominal fat tissue from myoma uteri
US-09-530-423-2

Query Match      21.5%  Score 293.5  DB: 4  Length 231.
Best Local Similarity 34.5%  Pred. No. 7.6e-22;
Matches 76;  Conservative 35;  Mismatches 78;  Indels 31;  Gaps 9.

OY  53  OGP-----PGPPGP-----PGIPGNNGNNNGATGHEGAKGKGDGD---LGPR---GE 97
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db   10  OGPGLVLPPLPGACCTGMMAGTIPGHHGHHGAGRGDRDGTPEKGEKGDPLGPRGDICE 69
      Matches 76;  Conservative 35;  Mismatches 78;  Indels 31;  Gaps 9.

OY-  98  RGOHQPKGEKGYPGI-----PPE---LQIAFMASLATHFSNONGIIFSSVEETNIGNF 147
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db   70  TGVPGAEPRGPRFGPGIOGRKKEGEGEAGAYVRSASFVGLETYVTIPMNPITFKTIFYNQNH 129

OY  148  FDMVTGRGCAVYSGYFFTFPSMKMKEDVEEYVYVLMHNGNYVFSMYSTEMKKSPTSSNH 207
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db   130  YDGSCTGKPHCNIPGLYFAYHITYV--KKDVVSLEFKDKAKLFTYDOYQENNVNDAAGS 187

OY  208  AVLKLAKGEVWLRLM-GNG---ALGHDRFSTFAGFLLE 243
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db   188  VLIHLEVGDQWLVQYEGEGRNGLIADNDNDSTFTGFLLY 227

RESULT 6
US-08-463-911-7
Sequence 7, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-911-7

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Query Match      21.5%: Score 293.5; DB 2; Length 244;
Best Local Similarity 34.5%: Pred. No. 8,2e-22;
Matches 76: Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGANGATGHEGAKGEKGDGD--LGPR--GE 97
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 23 QGPGLVLPRLPGKACTGMMAGIPIGRHNGHNGARCGRDRDGTPEKGEKGDPLIGPKDIGE 82

QY 98 RGOHPRKEKGYPGI-----PPE----LQIAFMASLATHTSNONGIIFSSVETNIGNF 147
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 83 TGVGAEEPRGPFPIQGRKKEGEGEAGAYVRSAFSGVLETVYTIIPMPRIFTKIFYNQNH 142

QY 148 FDMVMGRGACAVSGYFFTFSSMKHEDVEEYVYLIMHNGNTVFSYSEMKGSPTSSNH 207
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 143 YDGSIGRKHCHNIPGLYTAHYHTIY--MKDKVSLFKKDKKMLFTYYDOYQENNDQASGS 200

QY 208 AVLKLAGDEVYLMR-GNG---ALHGDHORESTFAGFLIF 243
   :  |  |||:::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 201 VLLHLEVGDYVWLQYVYGEGERNGLYADNDNDSTFGFLY 240

RESULT 7
US-09-140-804-3
; Sequence 3, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140, 804
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056, 983
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-804-3

Query Match      21.5%: Score 293.5; DB 4; Length 244;
Best Local Similarity 34.5%: Pred. No. 8,2e-22;
Matches 76: Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGANGATGHEGAKGEKGDGD--LGPR--GE 97
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 23 QGPGLVLPRLPGKACTGMMAGIPIGRHNGHNGARCGRDRDGTPEKGEKGDPLIGPKDIGE 82

QY 98 RGOHPRKEKGYPGI-----PPE----LQIAFMASLATHTSNONGIIFSSVETNIGNF 147
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 83 TGVGAEEPRGPFPIQGRKKEGEGEAGAYVRSAFSGVLETVYTIIPMPRIFTKIFYNQNH 142

QY 148 FDMVMGRGACAVSGYFFTFSSMKHEDVEEYVYLIMHNGNTVFSYSEMKGSPTSSNH 207
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 143 YDGSIGRKHCHNIPGLYTAHYHTIY--MKDKVSLFKKDKKMLFTYYDOYQENNDQASGS 200

QY 208 AVLKLAGDEVYLMR-GNG---ALHGDHORESTFAGFLIF 243
   :  |  |||:::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 201 VLLHLEVGDYVWLQYVYGEGERNGLYADNDNDSTFGFLY 240

RESULT 8
US-09-336-536-20
; Sequence 20, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Lelby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

```

```
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-20

Query Match
Best Local Similarity 34.5%; Score 293.5; DB 4; Length 244;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKGDGD---LGPR---GE 97
D 23 QGPVLLPLPFGACTGMMAGIPGHPGNHNGARCDRCDTGPCKGKGPGLIGPKGDIGE 82
QY 98 RGQGPCKGKGPCT-----PPE-----LQIAFMASLATHFSNONSGIIFSSVETNIGNF 147
D 83 TGVPAEBGPGRPGIQQGKGEGBGAYVRSFVSGLETVYTPMPPIRFTKIFYNQONH 142
QY 148 FDMVTGRFGAIVSGVYFFTFSMKHEDEYVYVLMHNGNTVFSMYSTEMKGSPTSNNH 207
D 143 YDGTGKHCNIPGLIYTAHHTYV--MKDVKVSLEFKDKKALFTYDQYQENNVDAAGS 200
QY 208 AVLKAKGDEYVLRM-GNG---ALHGDHQRSTFAGFLF 243
D 201 VLLHLEVGDYVWLQYVYGGERNGLYADNDNDSTFTGFLLY 240

RESULT 9
US-09-530-423-1
Sequence 1, Application US/09530423
Patent No. 6461821
GENERAL INFORMATION:
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
TITLE OF INVENTION: therefor
FILE REFERENCE: P98-51
CURRENT APPLICATION NUMBER: US/09/530,423
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: JP H9-297569
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 244
TYPE: PRT
ORGANISM: Abdominal fat tissue from myoma uteri
US-09-530-423-1

Query Match
Best Local Similarity 21.5%; Score 293.5; DB 4; Length 244;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKGDGD---LGPR---GE 97
D 23 QGPVLLPLPFGACTGMMAGIPGHPGNHNGARCDRCDTGPCKGKGPGLIGPKGDIGE 82
QY 98 RGQGPCKGKGPCT-----PPE-----LQIAFMASLATHFSNONSGIIFSSVETNIGNF 147
D 83 TGVPAEBGPGRPGIQQGKGEGBGAYVRSFVSGLETVYTPMPPIRFTKIFYNQONH 142
QY 148 FDMVTGRFGAIVSGVYFFTFSMKHEDEYVYVLMHNGNTVFSMYSTEMKGSPTSNNH 207
D 143 YDGTGKHCNIPGLIYTAHHTYV--MKDVKVSLEFKDKKALFTYDQYQENNVDAAGS 200
QY 208 AVLKAKGDEYVLRM-GNG---ALHGDHQRSTFAGFLF 243
D 201 VLLHLEVGDYVWLQYVYGGERNGLYADNDNDSTFTGFLLY 240
```

```
RESULT 10
US-09-140-804-8
Sequence 8, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-09-140-804-8

Query Match
Best Local Similarity 21.0%; Score 287; DB 4; Length 247;
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;

QY 6 LIYWQLALFLPFCLODEYVESPTGG--LPPDCSKCHGDVSRFGYGPGRPGPG 63
D 2 LLLQALLFLFLILP--SHARDVTTTEELAPALVPPKGTCA-----GMMA-----GIPG 48
QY 64 IPGNHNGNNGATGHEGAKGKGDGDPGRGER---GQGPCKGKGP-----GTP 114
D 49 HPGHNGTPGRDGRDGTPECKEKGDAGLLGPKGEGDVGMGABGPPGPOTPCGKKGPG 108
QY 115 E-----LQIAFMASLATHFSNONSGIIFSSVETNIGNFDMVTGRFGAIVSGVYFFTFSGM 170
D 109 EAATVYRAFAFVSGLETRTVNVPPIRFTKIFYNQONHNDGSKTKYCNIPGLIYVSHIT 168
QY 171 KHEDEYVYVLMHNGNTVFSMYSTEMKGSPTSNNHVLKAKGDEYVLRM-GNG---A 226
D 169 VY--MKDVKVSLEFKDKKAVLEFTYDQYQEKVNDOAGSVLLHLEVGDYVWLQYVYGGDHNH 226
QY 227 LHGDHQRSTFAGFLF 243
D 227 LYADNVNDSTFTGFLLY 243

RESULT 11
US-09-118-408-3
Sequence 3, Application US/09118408A
Patent No. 6265544
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapien
US-09-118-408-3

Query Match
Best Local Similarity 21.0%; Score 287; DB 4; Length 247;
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;

QY 6 LIYWQLALFLPFCLODEYVESPTGG--LPPDCSKCHGDVSRFGYGPGRPGPG 63
```

```
Db 2 LLLALLFLILP-SHADDVTTEELAPALVPPKGTCA-----GMAA-----GIPG 48
OY 64 IPGNNGNNGNNGATGHEGAKGEGKDGPRGER---GQGPKEGKYP-----GIPP 114
Db 49 HPHNGTGRGROGTPEKEGKDGAGLLGPKGEGDVGMGAGPKEPOTPGRKGPBG 108
OY 115 E-----LQIAFMASLATHFSNONGSIFFSVETNIGNFDMVTGGRFAPVSGVFFETFSM 170
Db 109 EAAVYKRSASFVSGLETRVTYVNVPRFKITFYNOONHDSGTGKFCYCNIPGLYFSYHIT 168
OY 171 KHEDEEYVYVLMHNGNTVFSMYSEMKKSDTSSNAVLKLAGDEWLMR-GNG---A 226
Db 169 VY--MKDVKVSILFKKDKAVLFTYDQYQEKNDVQASGVLLHLEVGDQVLMQVYGGDHNG 226
OY 227 LHGHORSTFAGFLIF 243
Db 227 LYADNVNDSTFTGFLLY 243
```

RESULT 12
US-09-506-855-3

```
; Sequence 3, Application US/09506855
; Patent No. 6448221
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Lasser, Gerald W.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
; FILE REFERENCE: 99-12
; CURRENT APPLICATION NUMBER: US/09/506,855
; CURRENT FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-506-855-3
```

Query Match 21.0%; Score 287; DB 4; Length 247;
Best Local Similarity 31.9%; Pred. No. 3.8e-21;
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;

```
OY 6 LIYQDALLFLPRLCDEYVESQGTG--LPPDCSKCHGDSFRGYQPPRPPGPG 63
Db 2 LLLALLFLILP-SHADDVTTEELAPALVPPKGTCA-----GMAA-----GIPG 48
OY 64 IPGNNGNNGNNGATGHEGAKGEGKDGPRGER---GQGPKEGKYP-----GIPP 114
Db 49 HPHNGTGRGROGTPEKEGKDGAGLLGPKGEGDVGMGAGPKEPOTPGRKGPBG 108
OY 115 E-----LQIAFMASLATHFSNONGSIFFSVETNIGNFDMVTGGRFAPVSGVFFETFSM 170
Db 109 EAAVYKRSASFVSGLETRVTYVNVPRFKITFYNOONHDSGTGKFCYCNIPGLYFSYHIT 168
OY 171 KHEDEEYVYVLMHNGNTVFSMYSEMKKSDTSSNAVLKLAGDEWLMR-GNG---A 226
Db 169 VY--MKDVKVSILFKKDKAVLFTYDQYQEKNDVQASGVLLHLEVGDQVLMQVYGGDHNG 226
OY 227 LHGHORSTFAGFLIF 243
Db 227 LYADNVNDSTFTGFLLY 243
```

RESULT 13
US-08-463-911-4
; Sequence 4, Application US/08463911
; Patent No. 5869330
; GENERAL INFORMATION:
; APPLICANT: Scherer, Philipp E.
; APPLICANT: Lodish, Harvey F.

```
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,911
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-9540
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-463-911-4
```

Query Match 20.0%; Score 274; DB 2; Length 246;
Best Local Similarity 31.3%; Pred. No. 7.6e-20;
Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;

```
OY 51 GYQPPRPPGPPGIPGNGNNGNNGATG-----EGAKGEGKDGDLGPRERORQPK 104
Db 32 GCYIGPMGPMGARGKKGKHDLOGPKGEPGIPAVPGGPGGEGPMGPKRKNR 91
OY 105 GEKGYGPIR-----DELO-----IAFMASLATHFSNONGSIFFSVETNIGNF 147
Db 92 GTSGLPDPPGPRGPGEGVEGRIYKQKQSVTVYTRQTTQYFANALVRFNSVYTNPOGH 151
OY 148 FDMVTGPRGAPVSGVFFETFSMKKHEDEEYVYVLMHNGNTVFSM-----SYEMK 198
Db 152 YNPSTGKFTCEVPLGYRYY-----YTSHTANLCVHLNMLARVASFCDIHF 198
OY 199 GKSDTSSNAVLKLAGDEWLMRGC--NGALHGHORSTFAGFLIF 243
Db 199 NSKQVSSGALLRLRGDEWLVNDYNGMV-GIEGSNSVFSGFLIF 244
```

RESULT 14
US-09-370-838-185
; Sequence 185, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Mohamath, Rodiah
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-185

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```

Query Match          20.0%; Score 273; DB 4; Length 746;
Best Local Similarity 29.6%; Pred. No. 4,4e-19;
Matches 72; Conservative 43; Mismatches 90; Indels 38; Gaps 8;

```

```

QY 34 GLPDCSKCCGHDYS-----FRGCGPP-----GPPGPGIGPNHNGNN 74
Db 509 GLP-----SISNGNTSGLQFOQAREYSGAPYSQRDNFQOCYKRGSTGCGPRANSRAGMSDSS 564
QY 75 GATGHEGAKGCKGDKDGLGPRGERGQ-----HGPKGE-----KGYGCIPELQIAFMAS 123
Db 565 QVSSPE--RDNETFNSGDSGQDSRSMTPVVDVPTNPATILPVHYV--LPQOMRVAFSA 622
QY 124 LATIFS--NONGSITFSVETINIGNFDVMTGRGAPYSGYFFTFPSMKHEDVEEYVY 181
Db 623 RTSNLAGETLDQPIVFDLLNMLGTFDLQGRNCPVNGTYVFIPIHMLKLAIVNPLYVN 682
QY 182 LMHNGNTVFSWYSYEMKGSPTSSNHAIVLKLAKGDEVYLRMGNGALHGDHOREFSTFAGEL 241
Db 683 LMKNEEVLVAIYANDGAPDHETASNAHILQLFOCDQITLRLRGAIYSSMKYSTFSGYL 742
QY 242 LFE 244
Db 743 LYQ 745

```

```

RESULT 15
US-09-336-536-4
; Sequence 4, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-4

```

```

Query Match          19.3%; Score 264.5; DB 4; Length 228;
Best Local Similarity 32.4%; Pred. No. 6.3e-19;
Matches 68; Conservative 36; Mismatches 79; Indels 27; Gaps 7;

```

```

QY 56 PGPPGPGIGPNHNGN-----NGNNGATGHEGAKGKGD-----KGDGPRGERGQ 100
Db 14 PGHPLPCTPGHHSQGLPGRGRDGRDGCAPGAPGCKGEGRPGLPGRDGPGRGEAGP 73
QY 101 HGPKGCKGYPICPELQIAFMASLATIHSNONGSITFSVETINIGNFDVMTGRGAPYS 160
Db 74 AGPTGPAGECVPPRSASARSRRPPSDAPLPFDRLVYNEDGHAIDATGKFTCOV 133
QY 161 GYFFTFPSMKHEDVEEYVY--LMHNGNTVFSWYSYEMKG--KSDTSSNHAIVLKLAKGD 216
Db 134 GYTFPAV-----HATYVRSALFDLVKNGESIASFPQF--FGGMPKPAISLGGAMVRLPEPD 188
QY 217 EVMLRMNG--ALHGHORESTFAGFLF 243
Db 189 QVWVGVGVDYIGIYASIKIDSTFSGFLVY 218

```

Search completed: January 15, 2003, 19:41:37
Job time : 37 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 15, 2003, 19:33:35 ; Search time 49 Seconds

(without alignments)
482.634 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MWMQLIYWLALFLPFC.....LHGDRHRSFTAGFLFETK 246

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293.5	21.5	244	2	JC4708
2	280.5	20.5	674	2	S23297
3	278.5	20.4	680	2	S31216
4	275	20.1	674	2	S13301
5	274	20.0	246	2	S29328
6	270	19.8	680	1	CGH01D
7	264.5	19.3	219	2	T14782
8	258.5	18.9	744	1	A34246
9	256.5	18.8	744	2	S15435
10	255	18.7	245	1	CIH00C
11	251.5	18.4	253	1	CIH208
12	251.5	18.4	744	1	S23298
13	249	18.2	635	2	A57131
14	248	18.1	743	1	S23779
15	239.5	17.5	245	2	S19018
16	236.5	17.3	253	2	S49158
17	231.5	16.9	253	2	I49560
18	226	16.5	423	2	A55797
19	219	16.0	245	1	CIH00A
20	216	15.8	920	2	A45748
21	215	15.7	992	2	T08772
22	211.5	15.5	366	2	S11449
23	210.5	15.4	423	2	A41207
24	208	15.2	2944	2	A54849
25	207.5	15.2	775	2	A61228
26	207.5	15.2	1349	2	I46103
27	203.5	14.9	1707	2	A33526
28	203.5	14.9	1712	1	CGH02B
29	202	14.8	215	2	B48150

30	201	14.7	215	2	C48150	hibernation-relate
31	197	14.4	171	2	A34493	collagen alpha 1(I)
32	196	14.3	224	2	A60032	cerebellin-like xl
33	195.5	14.3	1315	2	A56101	collagen alpha 1(X)
34	195.5	14.3	1774	2	B56101	collagen alpha 1(X)
35	193.5	14.2	1744	2	S40991	collagen alpha 1(I)
36	193	14.1	296	2	A31219	collagen 1 - Caeno
37	193	14.1	301	2	T21314	hypothetical prote
38	192.5	14.1	921	2	S42617	collagen alpha 1(I)
39	192	14.0	1466	1	CGH07L	collagen alpha 1(I)
40	190.5	13.9	289	2	T26812	hypothetical prote
41	189	13.8	193	2	A37873	cerebellin precus
42	189	13.8	375	1	A45225	pulmonary surfacta
43	189	13.8	1464	2	S59856	collagen alpha 1(I)
44	187.5	13.7	921	2	S40495	collagen alpha 1(I)
45	187	13.7	684	2	A53019	collagen alpha 1(X)

ALIGNMENTS

RESULT 1

JC4708 gelatin-binding 28K protein precursor - human

N:Alternate names: adipose specific collagen-like factor

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence #revision 19-Jul-1996 #text change 20-Sep-1999

C:Accession: JC4708; JC4944

R:Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.

Biochem. Biophys. Res. Commun. 221, 286-289, 1996

F:Title: cDNA cloning and expression of a novel adipose specific collagen-like factor

A:Reference number: JC4708; MUID:96224171; PMID:8619847

A:Accession: JC4708

A:Molecule type: mRNA

A:Residues: 1-244 <NAE>

A:Cross-references: DBJ:D45371; MID:9871886; PIDN:BA08227.1; PID:9871887

A:Experimental source: adipose tissue

R:Nakano, Y.; Tohe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M.

J. Biochem. 120, 803-812, 1996

A:Title: Isolation and characterization of G8P28, a novel gelatin-binding protein pur

A:Reference number: JC4944; MUID:97103474; PMID:8947845

A:Accession: JC4944

A:Molecule type: protein

A:Residues: 19-38;93-100;101-112;135-149;173-178 <NAK>

C:Comment: This protein is an endogenous factor that binds with a collagen-like domai

C:Genetics:

A:Gene: apm1

C:Superfamily: unassigned collagens; complement C1q carboxyl-terminal homology

C:Keywords: adipose tissue; glycoprotein; hydroxyproline

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-244/Product: gelatin-binding 28kDa protein #status experimental <MAT>

F:42-107/Region: collagen-like

F:114-241/Domain: complement C1q carboxyl-terminal homology <C1Q>

F:95/Modified site: 4-hydroxyproline (Pro) #status experimental

F:230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 21.5%; Score 293.5; DB 2; Length 244;

Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY	53	QGP----	PGPPG-----	PGIPGNHNGNNGATGHEGAKGKGDGD--	LGPR--GE	97
DB	23	QGGVLLPLP	KGACCTGMMAGITPRPHNGNPGDGDGTFGKGEKGDPELLPKGDICE	82		
QY	98	RGQHGKKEKGYPGI-----	PPE----	LQIAFMASLATHFSNONGIIFSSVETNIGNF	147	
DB	83	TGVPGAGEGPRGEPGIGCRKCEPGECAVYVRSAPSVLETFVTLPNMPIRTKTFYMOQNH	142			
QY	148	FDVMTGRFGAPGCVGYFFFSMMKHEDVEVYVYLMHNGTFSVSMYSKKGKSDSSNH	207			
DB	143	YDSTGRFHCNIPGLYFAHITVY--	MKDVKVSLEKRRKRAMLFTTDQYQENNVDAQSSG	200		
QY	208	AVLKLAKGDEVLMR-GNG--	ALHGDRHRSFTAGFLFLF	243		

Db 503 EGELEPPPPPPGQAVMPDGFIRAGORPLSGMPLVSNHCYTMPVSAFTVILSKAY 562
 QY 129 SNQNSGIIFSSVETNIGNEFDVWTGRFGAPVSGVYFFTFSMKHEDVEEYVYLHNGMT 188
 Db 563 PAVGADIPFDELLYNQOHYDPRSGIFTCIKPIYIEFHV--HVKGTHVWGLYKNGRP 620
 QY 189 VISMYSYE--MGKSTSSNHAVALKLAKGDEVYLRMGN---GALHDDHOFSTFAFLL 242
 Db 621 --TWMTYDEKSYSGYLDQASGSAIMELTENDQVWLQPLNAMESNGLYSSEYVHSSFSGLFV 677

RESULT 4

S13301

collagen alpha 1(X) chain precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999

C:Accession: S13301

R:Thomas, J. T.; Kwan, A. P. L.; Grant, M. E.; Boot-Handford, R. P.

Biochem. J. 273, 141-148, 1991

A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. EV

A:Reference number: S13301; MUID:91113131; PMID:1703407

A:Accession: S13301

A:Molecule type: mRNA

A:Residues: 1-674 <THO>

A:Cross-references: EMBL:X53556; NID:9263; PIDN:CAA37624.1; PID:9264

C:Genetics:

A:Gene: COL10A1

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer

F:1-18/Domain: signal sequence #status predicted <SIS>

F:19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>

F:547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 20.1%; Score 275; DB 2; Length 674;

Best Local Similarity 30.0%; Pred. No. 6-6e-15;

Matches 72; Conservative 31; Mismatches 87; Indels 50; Gaps 6;

QY 51 GYQGPPEPPGPGIPGNHGNNGNNGATGHEGAKGEKD-----KGDLGPRGERG 99
 Db 434 GHNGEAGPRGVPICPTGRGIPGPGIPGFGSGKDVGTGPPGAGIAYGLNGLPGP 493
 QY 100 QHCKREKGYPCIP-----PELQIA-----FMASLATHSSNONGSI 136
 Db 494 PPGKRNAGEPPGIPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG 553
 QY 137 -----FSSVETNIGNEFDVWTGRFGAPVSGVYFFTFSMKHEDVEEYVYLH 185
 Db 554 KAVPAIGTPIPFKILYKNOQHYDPRSGIFTCIKPIYIEFHV--HVKGTHVWGLYK 611
 QY 186 GNTVFESMYSEMKKSDTSSNHAVALKLAKGDEVYLRM---GNGALHGDHOFSTFA 242
 Db 612 GTFVMTYDEYIKGYLDQASGSAVIDLTENDQVWLQPLNAMESNGLYSSEYVHSS 671

RESULT 5

S29328

complement subcomponent C1q chain C - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

C:Accession: S29328

R:Petty, F.; Reid, K. B. M.; Loos, M.

Eur. J. Biochem. 209, 129-134, 1992

A:Title: Isolation, sequence analysis and characterization of cDNA clones coding for the

eCerebellin.

A:Reference number: S29328; MUID:93011118; PMID:1396691

A:Accession: S29328

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-246 <PET>

A:Cross-references: EMBL:X66295; NID:950228; PIDN:CAA46993.1; PID:950222

C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom

F:122-245/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 20.0%; Score 274; DB 2; Length 246;
 Best Local Similarity 31.3%; Pred. No. 2.8e-15;
 Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;

QY 51 GYQGPPEPPGPGIPGNHGNNGNNGATG-----EGAGKEGDKDGLGPRGERGONPK 104
 Db 32 GCYIGPGMCMGAPKDKDHDGLQKGERGIPAVYGTGQPKQKQKQKQKQKQKQKQK 91
 QY 105 GEKGYPCIP-----PELQIA-----FMASLATHSSNONGSIIFSSVETNIGNF 147
 Db 92 GTSGLPDEGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP 151
 QY 148 FDVMTGRFGAPVSGVYFFTFSMKHEDVEEYVYLHNGNTVFSM-----YSEMK 198
 Db 152 YNPSTGKFLCEVPGIYFYFY-----YTSHTANLVCVHLNMLARVASFCDHMF 198
 QY 199 GKSDDSSNHAVALKLAKGDEVYLRM---GNGALHDDHOFSTFAFLLF 243
 Db 199 NSKQVSSGALLRLQRGDEVYLSVNDYNGMV-GIEGSSNVFSGFLLF 244

RESULT 6

CGHUID

collagen alpha 1(X) chain precursor - human

N:Alternate names: procollagen alpha 1(X) chain

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999

C:Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856

R:Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B. R.; von der Mark, K.; Bertling,

FEBS Lett. 311, 305-310, 1992

A:Title: Genomic organization and full-length cDNA sequence of human collagen X.

A:Reference number: S26396; MUID:93012005; PMID:1397333

A:Accession: S26396

A:Molecule type: DNA

A:Residues: 1-680 <REI>

A:Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714; GB

R:Appte, S.S.

submitted to the EMBL Data Library, March 1992

A:Reference number: S30085

A:Accession: S30086

A:Molecule type: DNA

A:Residues: 'TTFYGVNVCVCLL', 52-680 <APT>

A:Cross-references: EMBL:X65120; NID:923129

A:Note: the initial difference is probably due to translation of an intronic sequence

R:Appte, S.; Mattei, M. G.; Olsen, B. R.

FEBS Lett. 282, 393-396, 1991

A:Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gen

A:Reference number: S15826; MUID:91243838; PMID:2037056

A:Accession: S15826

A:Molecule type: DNA

A:Residues: 561-647, 'G', 649-666 <AP2>

A:Cross-references: EMBL:X58879; NID:930013; PIDN:CAA41686.1; PID:930014

R:Thomas, J. T.; Cresswell, C. J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant

Biochem. J. 280, 617-623, 1991

A:Title: The human collagen X gene. Complete primary translated sequence and chromoso

A:Reference number: S18249; MUID:92109659; PMID:1764025

A:Accession: S18249

A:Molecule type: DNA

A:Residues: 1-26, 'T', 28-680 <THO>

A:Cross-references: EMBL:X60382; NID:930094; PIDN:CAA42933.1; PID:930095

A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-

R:Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.

Dev. Biol. 148, 562-572, 1991

A:Title: In situ hybridization studies on the expression of type X collagen in fetal

A:Reference number: A43901; MUID:92077285; PMID:1743401

A:Accession: A43901

A:Molecule type: mRNA

A:Residues: 547-656 <RE2>

A:Cross-references: GB:M74050; GB:D57494; NID:9339884; PIDN:AAA61221.1; PID:9553796

A:Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIIP:69014)

R:Wallis, G. A.; Rash, B.; Sweetman, W. A.; Thomas, J. T.; Super, M.; Evans, G.; Grant,

Am. J. Hum. Genet. 54, 169-178, 1994

A:Title: Amino acid substitutions of conserved residues in the carboxyl-terminal doma

pe Schmid
 A:Reference number: 151870; MUID:94136476; PMID:8304336
 A:Accession: 151870
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 520-597; 'D', 599-680 <MAL>
 A:Cross-references: GB:S66531; NID:9545180; PID:NAC0615.1; PID:545181
 A:Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
 C:Comment: a second mutant sequence with 614-pro is also described
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 ed and subsequently O-glycosylated.
 C:Genetics:
 A:Gene: GDB:COL0A1
 A:Cross-references: GDB:128635; OMIM:120110
 A:Map position: 6q21-q22
 A:Introns: 52/1
 A:Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia
 C:Complex: type X collagen may be a homotrimer
 C:Function:
 A:Description: structural component of extracellular fibrous polymer specifically and th
 be important for skeletogenesis
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine;
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-56/Domain: amino-terminal nonhelical #status predicted <MAT>
 F:57-519/Region: interrupted helical
 F:520-680/Domain: amino-terminal nonhelical #status predicted <NC1>
 F:553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
 F:617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.8%; Score 270; DB 1; Length 680;
 Best Local Similarity 28.5%; Pred. No. 1.7e-14;
 Matches 75; Conservative 28; Mismatches 102; Indels 58; Gaps 6;

QY 34 GLPPDCSKCHGDSYFRGYPGPPGPIGNHNGNNGATGHEGAKGKGD----- 88
 DB 419 GLRPPGPA--GAKGPHGNGEAGPRGAPGIRPGRIPGPIRGSGDPCSGPPG 476
 QY 89 -----KGLGPRGERGQHGPKGKGYPGIP-----PELQ- 117
 DB 477 PAGIATKGLNGPGRPGPRGSGEPGLPGRPPGQAUMEGRFKAGQRPRLSG 536
 QY 118 -----IAFMASLATHFSNONGSIIFSSVENIGNFEDVMTGRGCAVSGV 162
 DB 537 TPVLSANQCVTGPASFTVILSKAIPALGPIPIPKILYNRQOHYDPTGIFTQIPGI 596
 QY 163 YFTFSMKHEDVEEYVYLMHNGNTVFSYSEMKGSDTSNNAVLAKGDEYWLRM 222
 DB 597 YFSTYV--HVKGNHWAVLLKNGTPVMTYDEYTKGIDQASGSAIIDLTDNDYWLQ 654
 QY 223 GN--GALGHDHQRSTFAGFL 242
 DB 655 PNAESNGLYSSEYVSSFGFLV 777

RESULT 7
 T14782
 hypothetical protein DKFZp586B0621.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
 C:Accession: T14782
 R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, August 1999
 A:Reference number: 218184
 A:Accession: T14782
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-219 <OT>
 A:Cross-references: EMBL:AL110261
 A:Experimental source: adult uterus; clone DKFZp586B0621
 C:Genetics:
 A:Note: DKFZp586B0621.1.

C:Superfamily: complement C1q carboxyl-terminal homology
 Query Match 19.3%; Score 264.5; DB 2; Length 219;
 Best Local Similarity 32.4%; Pred. No. 1.5e-14;
 Matches 68; Conservative 36; Mismatches 79; Indels 27; Gaps 7;

QY 56 PGRPPGPIGNGN-----KGNNGATGHEGAKGKGD-----KGLGPRERQ 100
 DB 5 PGRHGLPTGTHGSGQLPGRDRDRDGAAPGKGGCGRPLGPRGDDPGRGAGP 64
 QY 101 HGRGKGYGIPPELOIAFMASLATHFSNONGSIIFSSVENIGNFEDVMTGRGAPVS 160
 DB 65 AGPTGAGGECVPRPASFARSRPSPDAPLPEDRVLYVDSGHYAVTKFTCYRP 124
 QY 161 GYVFTFSMKHEDVEEYVY--LMHNGTVFSYSEMKG--KSDTSSNNAVLAKGD 216
 DB 125 GYVYFAV---HATVYRASLPDLVKNKGESIAFFQF--FGGWPKPASLSGAWVRLEPD 179
 QY 217 EYVLRMGNG---ALHGDHQRSTFAGFL 243
 DB 180 QVWVQVGVGDYIGIVASIKTDSFGFLV 209

RESULT 8
 A34246
 collagen alpha 1(VIII) chain precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A34246
 R:Yamaguchi, N.; Benay, P.D.; van der Rest, M.; Nioomiya, Y.
 J. Biol. Chem. 264, 16022-16029, 1989
 A:Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that t
 omins similar to those of type X collagen.
 A:Reference number: A34246; MUID:89380199; PMID:2476437
 A:Accession: A34246
 A:Molecule type: mRNA
 A:Residues: 1-744 <RAM>
 A:Cross-references: GB:J05042; NID:9164895; PID:AAA1204.1; PID:9164896
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
 F:21-117/Region: amino-terminal nonhelical
 F:118-571/Region: interrupted helical
 F:572-744/Region: carboxyl-terminal nonhelical
 F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 18.9%; Score 258.5; DB 1; Length 744;
 Best Local Similarity 30.3%; Pred. No. 1.7e-13;
 Matches 79; Conservative 24; Mismatches 103; Indels 55; Gaps 6;

QY 34 GLPPDCSKCHGDSYFRGYPGPPGPIGNHNGNNGATGHEGA-----KGE 85
 DB 486 GLPGD--QGLOGPPGPIGPIGPIGPKGEPGLPGRPPGKPVAGLHGP 543
 QY 86 KDKKDLGPRGERGQHGPKGKGYPGIP-----PELQ- 118
 DB 544 PGRGALGPGGGLPGRPPGPPGPAVMPPTPAPOGEYLPDMGLGIDGVTPHAYAA 603
 QY 119 -----AFMASLATHFSNONGSIIFSSVENIGNFEDVMTGRGCAVSGV 165
 DB 604 KRKKNQPRAYEMAFRLALTPPPGAPRIKPRLLLYNQRONTNPOTGTGTCVPPVYTF 663
 QY 166 TFSMKHEDVEEYVYLMHNGNTVFSYSEMKGSDTSNNAVLAKGDEYWLRM- 224
 DB 664 AYHV--HCKGNVWVALLKNEPVMYTYDEYKGFIDQASGSAVLLLRGDRVFLQMPSE 721
 QY 225 --GALGHDHQRSTFAGFL 243
 DB 722 QAAGLYAGQYVHSSFGFLY 742

RESULT 9
 S15435

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 15, 2003, 18:56:40 ; Search time 38 Seconds
(without alignments)
268.505 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367
Sequence: 1 MAMROLIYQQLALFLFLPFC.....LHGDRPSPAGFLFETK 246

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	100.0	246	1 COR3_HUMAN	O99xj4 homo sapien
2	315	23.0	289	1 COR7_HUMAN	O99xj2 homo sapien
3	304	22.2	285	1 COR2_HUMAN	O99xj5 homo sapien
4	297.5	21.8	258	1 C1RF_HUMAN	O75973 homo sapien
5	297.5	21.8	258	1 C1RF_MOUSE	O88992 mus musculu
6	294	21.5	247	1 APM1_MOUSE	O60994 mus musculu
7	293.5	21.5	244	1 APM1_HUMAN	O15848 homo sapien
8	289.5	21.2	278	1 COR6_HUMAN	O99x19 homo sapien
9	285.5	20.9	255	1 GLIC_MOUSE	O96sn4 mus musculu
10	280.5	20.5	674	1 CA1A_CHICK	P08125 gallus gall
11	278.5	20.4	680	1 CA1A_MOUSE	O05306 mus musculu
12	275	20.1	674	1 CA1A_BOVIN	P23206 bos taurus
13	274	20.0	246	1 C1OC_MOUSE	O02105 mus musculu
14	270	19.8	680	1 CA1A_HUMAN	O03692 mus sapien
15	264.5	19.3	243	1 COR5_HUMAN	O99xj0 homo sapien
16	258.5	18.9	744	1 CA18_RABIT	P14282 oryctolagus
17	257.5	18.8	744	1 CA18_HUMAN	P27658 homo sapien
18	257	18.8	743	1 C1A8_MOUSE	O00780 mus musculu
19	255	18.7	245	1 C1OC_HUMAN	P02747 homo sapien
20	254	18.6	419	1 COLE_LEPMA	P98085 leptomys mac
21	251.5	18.4	251	1 C1OB_HUMAN	P02746 homo sapien
22	249	18.2	635	1 CA28_HUMAN	P25067 homo sapien
23	239.5	17.5	245	1 C1OA_MOUSE	P98086 mus musculu
24	236.5	17.3	253	1 C1OB_RAT	P31721 rattus norv
25	231.5	16.9	253	1 C1OB_MOUSE	P14106 mus musculu
26	226	16.5	281	1 COR1_HUMAN	O99xj1 homo sapien
27	219	16.0	245	1 C1QA_HUMAN	P02745 homo sapien
28	211.5	15.5	366	1 CAS4_EPHMU	P18503 ephydalia m
29	208	15.2	2944	1 CA17_HUMAN	O02388 homo sapien
30	203.5	14.9	1707	1 CA24_MOUSE	P08122 mus musculu
31	203.5	14.9	1712	1 CA24_HUMAN	P08572 homo sapien
32	202	14.8	215	1 HP25_TAMSI	O06576 tamias sibi
33	201	14.7	215	1 HP27_TAMSI	O06577 tamias sibi

34	200	14.6	1516	1 CA1H_HUMAN	P39060 homo sapien
35	196	14.3	224	1 CERL_RAT	P98087 rattus norv
36	195.5	14.3	1527	1 CA1H_MOUSE	P39061 mus musculu
37	195	14.2	458	1 COLO_RAT	O35167 rattus norv
38	193.5	14.2	1758	1 CA14_CAEEL	P17139 caenorhabd1
39	193	14.1	296	1 CC01_CAEEL	P08124 caenorhabd1
40	193	14.1	456	1 CO1Q_HUMAN	O99215 homo sapien
41	192	14.0	1466	1 CA13_HUMAN	P02461 homo sapien
42	189	13.8	193	1 CERB_HUMAN	P23435 homo sapien
43	189	13.8	193	1 CERB_MOUSE	O9171 mus musculu
44	189	13.8	375	1 PSPD_HUMAN	P35247 homo sapien
45	189	13.8	1464	1 CA13_MOUSE	P08121 mus musculu

ALIGNMENTS

RESULT 1
COR3_HUMAN STANDARD: PRT: 246 AA.
AC O99xj4; O96KY1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Complement-clq tumor necrosis factor-related protein 3 precursor
DE (Secretory protein COR326).
GN C1QTNF3 OR CTRP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Piddington C.S., Bishop P.;
RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Maeda T., Hayashi A., Saito T.;
RT "Molecular cloning, chromosomal localization, and genomic structure of
RT the human COR326 gene.";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 121-246 FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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DR EMBL: AF329837; AAK17961.1;
DR EMBL: AF326976; AAK70344.1;
DR EMBL: BC016021; AAH16021.1;
DR Genew: HGNC:14326; C1QTNF3.
DR InterPro: IPR001073; C1Q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF01391; Collagen.1.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q.1.
DR PROSITE: PS01113; C1Q.1.
DR Collagen; signal.
FT SIGNAL 1 22
FT CHAIN 23 246
FT POTENTIAL.
FT COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
FT RELATED PROTEIN 3.

FT DOMAIN 51 113 COLLAGEN-LIKE.
 KW DOMAIN 114 246 C1Q.
 FT CONFLICT 214 214 K -> E (LN REF. 3).
 SQ SEQUENCE 246 AA: 26994 MW: C389B6C3A/3E5D29 CRC64;
 Query Match 100.0%; Score 1367; DB 1; Length 246;
 Best Local Similarity 100.0%; Pred. No. 1.6e-108;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMROLYIQLLAFLPCLCODEYMESPQTGGLPPDCSKCHGDSFRGYPGPPPG 60
 DB 1 MIMROLYIQLLAFLPCLCODEYMESPQTGGLPPDCSKCHGDSFRGYPGPPPG 60
 QY 61 PGKIPENHNGNNGATGHEGAKGEGKDGDLGPRGERGQHGPKEGYPGLPELQIAF 120
 DB 61 PGKIPENHNGNNGATGHEGAKGEGKDGDLGPRGERGQHGPKEGYPGLPELQIAF 120
 QY 121 MASLATHFNSNGSGLIFSSVETNIGNFPDMTGRGAPVSGYVFFFSMMKHEDVEEVY 180
 DB 121 MASLATHFNSNGSGLIFSSVETNIGNFPDMTGRGAPVSGYVFFFSMMKHEDVEEVY 180
 QY 181 YLMHNGNTVFSMYSTEMKCKSDTSSNHAVLKLAKGDEVLMRGNGALHGDHORESTFAGF 240
 DB 181 YLMHNGNTVFSMYSTEMKCKSDTSSNHAVLKLAKGDEVLMRGNGALHGDHORESTFAGF 240
 QY 241 LLEETK 246
 DB 241 LLEETK 246

RESULT 2
 COT2_HUMAN STANDARD: PRT: 289 AA.
 ID COT2_HUMAN STANDARD: PRT: 289 AA.
 AC 09BXJ2;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Complement-c1q tumor necrosis factor-related protein 7 precursor.
 GN C1QTNF7 OR CTRP7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.;
 RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";
 RN Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
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DR EMBL: AF329839; AKI1963.1;
 DR EMBL: BC022187; AAH22187.1;
 DR Genew: HGNC:14342; C1QTNF7.
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; C1q; 1.
 DR Pfam: PF01391; Collagen; 2.
 DR PRINTS: PRO0007; COMPLEMENTC1Q.
 DR SMART: SM00110; C1Q; 1.

DR PROSITE: PS01113; C1Q; 1.
 KW Collagen; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 289
 FT DOMAIN 38 139
 FT DOMAIN 141 276
 FT SEQUENCE 289 AA: 30683 MW: A61609FF8D26946 CRC64;
 Query Match 23.0%; Score 315; DB 1; Length 289;
 Best Local Similarity 30.1%; Pred. No. 1.3e-19;
 Matches 86; Conservative 32; Mismatches 96; Indels 72; Gaps 9;

QY 14 LFLPLPCLCODEYMESPQTGGLPPDCSKCHGDSFRGYPGPPPGIPENHNGN 73
 DB 5 LVTSTALICASGPRGNQLKGENYSPRYIC---SLPGLGPPGPGCANSPGPHRIGL 60
 QY 74 NCATGHEGAKGEGKDGDLGPRGERGQHGPKEGYPGLPELQIAF 103
 DB 61 PGKIPENHNGNNGATGHEGAKGEGKDGDLGPRGERGQHGPKEGYPGLPELQIAF 120
 QY 104 -----KGEKYPGIPP-----ELQIAFMASLATHFNSNGSGLIFSSVETNIGNFPDV 150
 DB 121 PGKIPENHNGNNGATGHEGAKGEGKDGDLGPRGERGQHGPKEGYPGLPELQIAF 180
 QY 151 MGRFGAPVSGYVFFFSMMKHEDVEEVYLMHNGNTVFSMYSTEMK-----CKS 201
 DB 181 ATGKFCAPFGIYFYSYDITLANKH-----LATGLVHNG-----QYRKTFDANTGNH 228
 QY 202 DTSSNHAVLKLAKGDEVLMRGNGALHGDHORESTFAGF 243
 DB 229 DVASGSTVIYLOPEDEVLMRGNGALHGDHORESTFAGF 274

RESULT 3
 COT2_HUMAN STANDARD: PRT: 285 AA.
 ID COT2_HUMAN STANDARD: PRT: 285 AA.
 AC 09BXJ5;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Complement-c1q tumor necrosis factor-related protein 2 precursor.
 GN C1QTNF2 OR CTRP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Piddington C.S., Bishop P.;
 RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";
 RN Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Muscle;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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DR EMBL: AF329836; AKI1960.1;
 DR EMBL: BC011699; AAH11699.1;
 DR Genew: HGNC:14325; C1QTNF2.
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.

```

DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 2.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Collagen; Signal.
FT SIGNAL 1 15
FT CHAIN 16 285
FT DOMAIN 40 141
FT DOMAIN 143 285
SQ SEQUENCE 285 AA; 29952 MW; 7E31FF9868D4EDFA CRC64;

Query Match 22.2%; Score 304; DB 1; Length 285;
Best Local Similarity 29.6%; Pred. No. 1,le-18;
Matches 73; Conservative 42; Mismatches 74; Indels 58; Gaps 9;

OY 48 SFRGQGPFGPPPP-----GIP---GNHGNNNGATGHEGANGKGDGLDPR 95
DB 37 SLPGFGPPGPGAGAPSGMGMGRMGFGPKGDGDGDHCDRSGSEGGPGRTGNRKGPGPK 96
OY 96 GER-----GOHGPKGEKGYPGIP-----PELQIAFMASL 124
DB 97 GKAGALGAGPGRPGKGVNGTPGKHGTGPKGKGGKGGELPGPCSCSGGHTKSAFSAVAV 156
OY 125 ATHESSNGSIIFSSVETNIGNFEDVMTGRFGAPYSGVYFFTFSSM---KHEDVEEYVY 181
DB 157 TKSYPRELPIKFKDILMNEGHNASSGKFCVGPAGIYFYFDITLANKH-----LAIG 211
OY 182 LMHNGNTVFSMTSEMK-GKSDTSSNAVLKLAGDEVWLRN-----GNCALGHDRST 236
DB 212 LVHNGO--YRIRTFDANGNHVAVSGSTILAKGDEVWLQIFVSEONGLFYDPYWTDSL 269
OY 237 FAGFLF 243
DB 270 FTGFLY 276

RESULT 4
C1RF_HUMAN STANDARD: PRT: 258 AA.
ID C1RF_HUMAN
AC 075973;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Clq-related factor precursor.
GN C1QRF OR CRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP MEDLINE=99097006; PubMed=9878755;
RX Berube N.G., Swanson X.H., Bertam M.J., Kittle J.D., Didenko V.,
RA Baskin D.S., Smith J.R., Pereira-Smith O.M.;
RT "Cloning and characterization of CRF, a novel Clq-related factor,
RT expressed in areas of the brain involved in motor function.";
RL Brain Res. Mol. Brain Res. 63:233-240(1999).
RN 12
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,
RA Nickerson D.A.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL TISSUE=Placenta;
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; AF095154; AAC64186.1; -
DR EMBL; AF410771; AAK95248.1; -
DR EMBL; BC008798; AAH08798.1; -
DR InterPro; IPR001073; Clqagen.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Collagen; Signal.
FT SIGNAL 1 16
FT CHAIN 17 258
FT DOMAIN 67 115
FT DOMAIN 123 258
SQ SEQUENCE 258 AA; 26452 MW; 52C51CDF59CAE2BF CRC64;

Query Match 21.8%; Score 297.5; DB 1; Length 258;
Best Local Similarity 34.2%; Pred. No. 3,5e-18;
Matches 76; Conservative 32; Mismatches 89; Indels 25; Gaps 8;

OY 29 SPQTGLPPDCKSCCHGDSYFRGYOGPPGPGPGIPGHNHNGNNGATGHEGANGKGD 88
DB 53 SQSGAPPP--STLVQPGPKGPGRTKGPDPGPPGPP-----GPPGVPGPKEKE 101
OY 89 KGDLPGRG--ERQHGPKGEKGYPGIPPELQIAFMASLATHSSNONG--IIFSSVETN 143
DB 102 PKPGPPGLPGAGSGGALSTATTYTP--RVAFYAGL-----KNPEGYEVLFDDVYN 154
OY 144 IGNFEDVMTGRFGAPYSGVYFFTFSS-MKHEDVEEYVYLMHNGNTVFSMTSEMKGSD 202
DB 155 LGNNYDAASGKFTCNIPGYFFTYHVMHNGCGTSMWADLCNGQVARSALINDAQNND 214
OY 203 TSSNAVLKLAGDEVWLRMGNCALH-GDHQRPSTFAGFLF 243
DB 215 YASNSVILHLDAGDEVFLKIDGKAHAGNSNRYSTFGFLY 256

RESULT 5
C1RF_MOUSE STANDARD: PRT: 258 AA.
ID C1RF_MOUSE
AC 086992;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Clq-related factor precursor.
GN C1QRF OR CRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE=99097006; PubMed=9878755;
RX Berube N.G., Swanson X.H., Bertam M.J., Kittle J.D., Didenko V.,
RA Baskin D.S., Smith J.R., Pereira-Smith O.M.;
RT "Cloning and characterization of CRF, a novel Clq-related factor,
RT expressed in areas of the brain involved in motor function.";
RL Brain Res. Mol. Brain Res. 63:233-240(1999).
RN 12
RP OF THE NERVOUS SYSTEM INVOLVED IN BRAINSTEM. MORE ABUNDANT IN AREAS
CC OF THE PONS AND THE RED NUCLEUS.
CC THE ACCESSORY OLIVARY NUCLEUS,
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF095155; AAC64187.1; .
DR MGD: MGI:1344400; C1qrl.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF003386; C1q; 1.
DR Pfam: PF01391; Collagen; 1.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
DR Collagen; Signal.
KW SIGNAL.
FT CHAIN 1 16 POTENTIAL.
FT DOMAIN 67 115 C1Q-RELATED FACTOR.
FT DOMAIN 123 258 COLLAGEN-LIKE.
SQ SEQUENCE 258 AA; 26485 MW; F776E2D306BDF763 CRC64;

Query Match 21.8%; Score 297.5; DB 1; Length 258;
Best Local Similarity 31.2%; Pred. No. 3; Se-18;
Matches 73; Conservative 36; Mismatches 76; Indels 49; Gaps 8;

QY 29 SPQGTGPPDCSCCHDYSFRYGQPPGPPGICPNHNGNNGATGHEGAKGKGD 88
Db 53 SEGSGAPP--STLVGQPGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGK 89
QY 89 KGDGPRERQHGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGKRGK 134
Db 90 PGVPGPEKGEKPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG 142
QY 135 --IIFSSVENINIGFVMTGREGAPVSGVYFFTES--MKHEVEEYVYLMHNGTVE 190
Db 143 KEVLKFDVYTNLGNNDYASGKFTCNIPGYFTYHLMGSGGTSMWALDCKNGQYRA 202
QY 191 SMYSYEMKSGSDTSSNAHVLKLAGDEYVLMNGALH-GDHQRFSPFAGFLP 243
Db 203 SAIQADADQNDVYASNSVYLHLDAAGDEVEIKLDGKKAHGKSNKSYSPFSGIT 256

RESULT 6
APM1_MOUSE STANDARD; PRT; 247 AA.
ID APM1_MOUSE 062400; 09DC68;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adiponectin precursor (30 kDa adipocyte complement-related protein)
DE (ACRP30) (Adipocyte specific protein Adipo).
GN APM1 OR ACRP30 OR ADIPOQ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE-Adipocyte;
RX MEDLINE=9607057; PubMed=7592907;
RA Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;
RT "A novel serum protein similar to C1q, produced exclusively in
RT adipocytes."
RL J. Biol. Chem. 270:26746-26749(1995).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE-Fibroblast;
RX MEDLINE=9620999; PubMed=8631877;
RA Hu E., Liang P., Spiegelman B.M.;

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RT "Adipo is a novel adipose-specific gene dysregulated in obesity."
RL J. Biol. Chem. 271:10697-10703(1996).
RN 13
RP SEQUENCE FROM N.A.
RX PubMed=11162643;
RA Das K., Lin Y., Widen E., Zhang Y., Scherer P.E.;
RT "Chromosomal localization, expression pattern, and promoter analysis
RT of the mouse gene encoding adipocyte-specific secretory protein
RT Acrp30."
RL Biochem. Biophys. Res. Commun. 280:1120-1129(2001).
RN 14
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinozawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner U., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN 15
RP FUNCTION.
RX MEDLINE=21372498; PubMed=11479627;
RA Yamauchi T., Kamon J., Waki H., Teranishi Y., Kubota N., Hara K.,
RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasao N., Ezaki O.,
RA Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,
RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
RA Froguel P., Kadowaki T.;
RT "The fat-derived hormone adiponectin reverses insulin resistance
RT associated with both lipodystrophy and obesity."
RL Nat. Med. 7:941-946(2001).
RN 16
RP FUNCTION.
RX MEDLINE=21372499; PubMed=11479628;
RA Berg A.H., Combs T.P., Du X., Brownlee M., Scherer P.E.;
RT "The adipocyte-secreted protein Acrp30 enhances hepatic insulin
RT action."
RL Nat. Med. 7:947-953(2001).
CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE
CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH
CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING
CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED
CC EXPRESSION OF ENDOTHelial ADHESION MOLECULES. INVOLVED IN THE
CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
CC -1- SUBUNIT: HOMODIGLIMER.
CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED EXCLUSIVELY BY ADIPOCYTES AND
CC SECRETED INTO SERUM.
CC -1- INDUCTION: DURING HORMONE-INDUCED ADIPOSE DIFFERENTIATION AND
CC ACTIVATED BY INSULIN.
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -----
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CC -----
 DR EMBL: U37222; AAA80543.1; -
 DR Mammalia; Eutheria; Primates; Carnivora; Euteleostomi;
 DR EMBL: U49915; AAB06706.1; -
 DR EMBL: AF304466; AAK13417.1; -
 DR EMBL: AK003138; BAB22597.1; -
 DR MGD; MGI:106675; AcP30.
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; C1q; 1.
 DR Pfam: PF01391; Collagen; 1.
 DR PRINTS: PRO0007; COLLAGEN1Q.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS0113; C1Q; 1.
 DR Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;
 KW Polymorphism.
 FT SIGNAL. 1 17 POTENTIAL.
 FT CHAIN 18 247 ADIPONECTIN.
 FT DOMAIN 45 110 COLLAGEN-LIKE.
 FT DOMAIN 111 247 C1Q.
 FT DISULFID 39 39 INTERCHAIN (BY SIMILARITY).
 FT MOD_RES 47 47 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 50 50 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 56 56 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 65 65 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 79 79 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 98 98 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 107 107 HYDROXYLATION (BY SIMILARITY).
 FT VARIANT 113 113 M -> V.
 FT CONFLICT 50 50 P -> S (IN REF. 2).
 FT CONFLICT 74 74 A -> S (IN REF. 2).
 FT CONFLICT 117 117 A -> G (IN REF. 2).
 FT CONFLICT 148 148 G -> N (IN REF. 2).
 FT CONFLICT 243 243 Y -> F (IN REF. 2).
 SQ SEQUENCE 247 AA: 26841 MM: 137B687D873988C4 CXC64;

Query Match 21.5%; Score 294; DB 1; Length 247;
 Best Local Similarity 31.5%; Pred. No. 6.5e-18;
 Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

QY 6 LIYQDLALFLPFLCQDEYVESPOTG--LPDSCSKCHDYFRYQGGPPGPPG 63
 DB 2 LLLQALLFLFLP-SHADDVTTTELAPALVPPKGTCA-----CWMA-----GIPIG 48
 QY 64 IPGNHNGNNGCATGHEGAKGKGDGLGPRGER---GQHGPKGKGYPGIPPE----- 115
 DB 49 HPGHNGTGRDRODGTPEKGEKGDAGLGPKEGTGDMGTGAEPPGPGPKKGEPC 108
 QY 116 ----LQIAFMASLATHFSNONGIIFSSVETNIGNFDMVTGRGAPVSGVYFFFSKM 170
 DB 109 EAAVYRASFVSGLETRVTPVPRPIRPIKIFYNQGNHDSGKRYCNPGLYFSYHIT 168
 QY 171 KHEDEEYVYVLMHNGVNFVSYEMKGSPTSSNHAVALKAKDEVALRN-GNG---A 226
 DB 169 VY--MKDVKVSLEFKDKRAVLFTYDQYQEKNVDOASGVLLHLEVDQWLAQYCGDGHNG 226
 QY 227 LHGDHQRSTFAGFLIF 243
 DB 227 LYADVNDSTFTGLLY 243

RESULT 7
 APM1_HUMAN STANDARD: PRT: 244 AA.
 AC Q15848;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Adiponectin precursor (30 kDa adipocyte complement-related protein)-
 DE (ACRP30) (Adipose most abundant gene transcript 1) (apm-1) (Gelatin-
 binding protein).
 GN APM1 OR ACRP30 OR GBP28.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Carnivora; Euteleostomi;
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Adipose tissue;
 RA MEDLINE=96224171; PubMed=8619847;
 RA Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y.,
 RA Matsubara K.;
 RT "cDNA cloning and expression of a novel adipose specific collagen-like
 factor, apm1 (Adipose Most abundant Gene transcript 1).";
 RL Biochem. Biophys. Res. Commun. 221:286-289(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99196984; PubMed=10095105;
 RA Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M.,
 RA Nakano Y., Shimizu N., Tomita M.;
 RT "Organization of the gene for gelatin-binding protein (GBP28).";
 RL Gene 229:67-73(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99333693; PubMed=10403784;
 RA Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Drobnik W.,
 RA Fuerst A., Scholmerich J., Schmitz G.;
 RT "The human apm-1, an adipocyte-specific gene linked to the family of
 TNF's and to genes expressed in activated T cells, is mapped to
 RT chromosome 1q21.3-q23, a susceptibility locus identified for familial
 RT combined hyperlipidemia (FCH).";
 RL Biochem. Biophys. Res. Commun. 260:416-425(1999).
 RN [4]
 RP CHARACTERIZATION.
 RA MEDLINE=20417747; PubMed=10961870;
 RA Yokota T., Oritani K., Takahashi I., Ishikawa J., Matsuyama A.,
 RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y.,
 RA Matsuzawa Y.;
 RT "Adiponectin, a new member of the family of soluble defense collagens,
 RT negatively regulates the growth of myelomonocytic progenitors and the
 RT functions of macrophages.";
 RL Blood 96:1723-1732(2000).
 RN [5]
 RP CHARACTERIZATION.
 RA MEDLINE=20440368; PubMed=10982546;
 RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,
 RA Hotta K., Nishida M., Muraguchi M., Takahashi M., Ohmoto Y.,
 RA Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Adiponectin, an adipocyte-derived plasma protein, inhibits
 RT endothelial NF-kappaB signaling through a C/EBP-dependent pathway.";
 RL Circulation 102:1296-1301(2000).
 RN [6]
 RP FUNCTION.
 RA MEDLINE=21372498; PubMed=11479627;
 RA Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K.,
 RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
 RA Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,
 RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
 RA Froguel P., Kadwaki T.;
 RT "The fat-derived hormone adiponectin reverses insulin resistance
 RT associated with both lipodystrophy and obesity.";
 RL Nat. Med. 7:941-946(2001).
 RN [7]
 RP VARIANT ADIPONECTIN DEFICIENCY CYS-112.
 RA MEDLINE=20378830; PubMed=10918532;
 RA Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K.,
 RA Hori M., Shimomura I., Hotta K., Kuriyama H., Nakamura T.,
 RA Yamashita S., Funahashi T., Matsuzawa Y.;
 RT "Genomic structure and mutations in adipose-specific gene,
 RT adiponectin.";
 RL Int. J. Obes. Relat. Metab. Disord. 24:861-866(2000).
 RN [8]
 RP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.
 RA MEDLINE=21671103; PubMed=11812766;
 RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,
 RA Otabe S., Okada T., Eto K., Kadwaki H., Hagiura R., Akanuma Y.,

RA Yasaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y.,
 RA Kimura S., Tomita M., Kimura S., Ito C., Froegel P., Kadowaki T.,
 RT "Genetic variation in the gene encoding adiponectin is associated with
 an increased risk of type 2 diabetes in the Japanese population.",
 RL Diabetes 51:536-540(2002).
 CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE
 CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH
 CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING
 CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED
 CC EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE
 CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
 CC -1- SUBUNIT: HOMODIGLIMER (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.
 CC -1- DISEASE: Defects in APOL are the cause of adiponectin deficiency,
 CC resulting in very low concentration of plasma adiponectin.
 CC decreased adiponectin plasma levels are associated with obesity
 CC insulin resistance, and diabetes type 2.
 CC -1- PHARMACEUTICAL: Adiponectin might be used in the treatment of
 CC diabetes type 2 and insulin resistance.
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
 CC -----
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 CC -----
 DR EMBL: DA5371; BAA08227.1; -
 DR EMBL: AB012165; BAA86716.1; -
 DR EMBL: AB012164; BAA86716.1; JOINED.
 DR EMBL: AJ131460; CAB52413.1; -
 DR EMBL: AJ131461; CAB52413.1; JOINED.
 DR MIM: 605441; -
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF003386; C1q; 1.
 DR Pfam: PF013391; Collagen; 1.
 DR PRINTS: PR00007; COMPLEMENTC1Q.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS01113; C1Q; 1.
 DR Hormone: Collagen: Signal; Repeat; Hydroxylation; Plasma:
 KW Polymorphism: Disease mutation; Obesity; Diabetes mellitus.
 FT SIGNAL 1 14
 FT CHAIN 1 244
 FT DOMAIN 42 107
 FT DISULFID 108 244
 FT MOD_RES 36 36
 FT MOD_RES 44 44
 FT MOD_RES 47 47
 FT MOD_RES 53 53
 FT MOD_RES 62 62
 FT MOD_RES 71 71
 FT MOD_RES 76 76
 FT MOD_RES 86 86
 FT MOD_RES 95 95
 FT MOD_RES 104 104
 FT VARIANT 84 84
 FT VARIANT 112 112
 FT VARIANT 117 117
 FT VARIANT 164 164
 FT VARIANT 221 221
 FT VARIANT 241 241
 FT SEQUENCE 244 AA; 26414 MW; 64D8C6C1204B1018 CRC64;

Query Match 21.5% Score 293.5; DB 1; Length 244;
 Best Local Similarity 34.5%; Pred. No. 7,1e-18;
 Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;
 QY 53 QGP-----PGPGP-----PGIPGNHNGNNGATGCGAGCKGDKD---LGRP---GE 97
 DB 23 QGPVLLPLPGAGCTAGMAGIPGHPGNAGAPGRDGTGCKEKEDKADPLGPKSGICE 82
 QY 98 RGQHPGPKGKPGI-----PPE---LQIAPMASLATPESNONSIIITSSVETNIGNF 147
 DB 83 TGVPGAGCPGPGFPGIQRKGPGEAGVYRSASFVSGLETVTTPNMPDIFRTKIPYNOOH 142
 QY 148 PDVWTGPGCAVSGVYFETSMKHEVVEEYVYVLMHNGNTVEMSYEAKGKSDTSNNH 207
 DB 143 YDSGTGFHCNIPGLYFAHITY--MKDVKSLEFKKRAMLETYDQYQENNVDAAGS 200
 QY 208 AVLKAGDEWVLRM-GNG---ALHGDHREFTAGLLE 243
 DB 201 VLHLVGDQVWLQVYGEGERNGILADNDSTFTGFLY 240
 RESULT 8
 ID COT6_HUMAN STANDARD; PRT; 278 AA.
 AC 09BX19;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Complement-c1q tumor necrosis factor-related protein 6 precursor.
 GN C1QTNF6 OR CTBP6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Piddington C.S., Sheppard P.O.;
 RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.",
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RC TISSUE=Placenta;
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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 CC -----
 DR EMBL: AE329842; AKI1966.1; -
 DR EMBL: BC020551; AAH20551.1; -
 DR Genew: HGNC:14343; C1QTNF6;
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF003386; C1q; 1.
 DR Pfam: PF013391; Collagen; 1.
 DR PRINTS: PR00007; COMPLEMENTC1Q.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS01113; C1Q; FALSE_NEG.
 KW Collagen; Signal.
 FT SIGNAL 1 46
 FT CHAIN 47 278
 FT DOMAIN 97 138
 FT DOMAIN 139 278
 FT CARBOHYD 91 91
 N-LINKED (GLCNAC...) (POTENTIAL).

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DR EMBL; M13496; AAA48736.1; ALT_SEQ.
 DR EMBL; J04194; AAA48634.1; -
 DR PIR; A31896; A31896.
 DR InterPro; IPR001073; C1q.
 DR InterPro; IPR000087; Collagen.
 DR Pfam; PF00386; C1q; 1.
 DR Pfam; PF01391; Collagen; 8.
 DR PRINTS; PR00007; COMPLEMENTC1Q.
 DR SMART; SM00110; C1Q; 1.
 DR PROSITE; PS01113; C1Q; 1.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Cartilage; Collagen; Signal.

FT SIGNAL 1 18
 FT CHAIN 1 674 COLLAGEN ALPHA 1(X) CHAIN.
 FT DOMAIN 19 52 NONHELICAL REGION (NC2).
 FT DOMAIN 53 512 TRIPLE-HELICAL REGION.
 FT DOMAIN 513 674 NONHELICAL REGION (NC1).
 FT DOMAIN 539 674 C1Q.
 FT MOD_RES 453 453 HYDROXYLATION.
 FT MOD_RES 456 456 HYDROXYLATION.
 SQ SEQUENCE 674 AA; 66434 MW; EAB48B1EF174B145 CRC64;

Query Match 20.5%; Score 280.5; DB 1; Length 674;
 Best Local Similarity 30.9%; Pred. No. 2.7e-16;
 Matches 76; Conservative 23; Mismatches 90; Indels 57; Gaps 5;

QY 51 GYGGPPGPPGPGIGGNGGNGGNGCATGHEGAKGEG-----DKGDLGPRGEG 99
 DB 427 GINGPGRGPRGPGIGGNGGNGGNGCATGHEGAKGEGAGAGLPGPAGIYTKGLRGMPGLG 486
 QY 100 QHPRGEGYPCIP-----PEIQI-----118
 DB 487 PPGPRGNGGEGPEIPGPPGPPGPGPGQSTIEGKESRELGSMPKAGANQALGMPVS 546
 QY 119 AFMAIAHFSNQNGSIIFFSVETNIGNFPDMTGRFGAPVSGYFFFTSMKHEDVEY 178
 DB 547 AFTVILSAVPCATVPVIFKDKILYRQOHYDPTGIFTCRPLGLYFSYHV--HAKGTNV 604
 QY 179 YYLNLNNTVFSMTSYEMKCKSDTSNNHAYLAKGDEVMRLMGN---GALHGHOHRS 235
 DB 605 WVALTKNKSPPWYTYDEYQKGLDQASGSAVIDLMENDQVWLQLPNSESNGLYSSEYHS 664
 QY 236 TFAGFL 241
 DB 665 SPSGFL 670

RESULT 11
 CAIA_MOUSE STANDARD: PRT: 680 AA.
 ID CAIA_MOUSE
 AC 005306;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Collagen alpha 1(X) chain precursor.
 GN COL10A1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RX MEDLINE=93143676; PubMed=8424763;
 RA Elima K., Eerola I., Rosati R., Metsaranta M., Garofalo S., Petrala M.,
 RA de Crombrughe B., Vuorio E.;
 RT "The mouse collagen X gene: complete nucleotide sequence, exon
 RT structure and expression pattern.";

RL Biochem. J. 289:247-253(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Liver;
 RX MEDLINE=93238750; PubMed=8477738;
 RA Kong R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,
 RA Grant M.E., Cheah K.S.E.;
 RT "Intron-exon structure, alternative use of promoter and expression of
 RT the mouse collagen X gene, Col10a-1.";
 RL Eur. J. Biochem. 213:99-111(1993).
 RN [3]
 RP SEQUENCE OF 51-680 FROM N.A.
 RC STRAIN=DBA/2J;
 RX MEDLINE=92267014; PubMed=1587271;
 RA Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.;
 RT "Cloning of the human and mouse type X collagen genes and mapping of
 RT the mouse type X collagen gene to chromosome 10.";
 RL Eur. J. Biochem. 206:217-224(1992).
 RN [4]
 RP SEQUENCE OF 385-627 FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=92182017; PubMed=1543751;
 RA Elima K., Metsaranta M., Kallio J., Petrala M., Eerola I.,
 RA Garofalo S., de Crombrughe B., Vuorio E.;
 RT "Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X)
 RT collagen mRNAs.";
 RL Biochim. Biophys. Acta 1130:78-80(1992).
 CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
 CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
 CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- PTM: PROLINES ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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DR EMBL; X67348; CAA47763.1; -
 DR EMBL; X65121; CAA46237.1; -
 DR EMBL; X63013; CAA44741.1; -
 DR EMBL; Z21610; CAA79736.1; -
 DR PIR; S28807; S28807.
 DR PIR; S31216; S31216.
 DR PIR; S22215; S22215.
 DR MGD; MGI:88445; Col10a1.
 DR InterPro; IPR001073; C1q.
 DR InterPro; IPR000087; Collagen.
 DR Pfam; PF00386; C1q; 1.
 DR Pfam; PF01391; Collagen; 9.
 DR PRINTS; PR00007; COMPLEMENTC1Q.
 DR PRODOM; PR00007; Collagen; 2.
 DR SMART; SM00110; C1Q; 1.
 DR PROSITE; PS01113; C1Q; 1.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Cartilage; Collagen; Signal.

FT SIGNAL 1 18
 FT CHAIN 1 680 POTENTIAL.
 FT DOMAIN 19 56 COLLAGEN ALPHA 1(X) CHAIN.
 FT DOMAIN 57 519 NONHELICAL REGION (NC2).
 FT DOMAIN 520 680 TRIPLE-HELICAL REGION.
 FT DOMAIN 545 680 NONHELICAL REGION (NC1).
 FT DOMAIN 248 248 C1Q.
 FT CONFLICT 286 286 P -> L (IN REF. 3).
 FT CONFLICT 286 286 A -> S (IN REF. 2).
 FT CONFLICT 306 306 L -> F (IN REF. 3).
 FT CONFLICT 417 417 T -> S (IN REF. 3).
 FT CONFLICT 451 451 R -> K (IN REF. 4).

FT CONFLICT 500 500 H -> L (IN REF. 3).
 FT CONFLICT 567 567 A -> C (IN REF. 3).
 FT CONFLICT 569 569 I -> H (IN REF. 3).
 FT CONFLICT 571 572 FD -> LY (IN REF. 3).
 FT CONFLICT 635 635 O -> T (IN REF. 3).
 SO SEQUENCE 680 AA: 66775 MW: FE984CA99AF708E2 CRC64:

Query Match 20.4%; Score 278.5; DB 1; Length 680;
 Best Local Similarity 30.5%; Pred. No. 4.1e-16;
 Matches 73; Conservative 34; Mismatches 87; Indels 45; Gaps 7;

QY 45 GDYSTRGQGPFGPPGPGPGIPGNGHNGNNGATG-----HEGAKGKDGKGLGPRGEG 99
 DB 443 GEPGIPGTRGPPGPGVPGFPGSKGDPGNPAGPAGIATKGLNPTGPPGPGRGHSG 502
 QY 100 QHGPKEGKGPICP-----PELQ-----IAPMASLATHF 128
 DB 503 EPGLPGRPPGPPGQAVMPDGFITAGORPRLSGMPLVSANNGVTGMPYSATFVILSKRY 562
 QY 129 SNQSGIIPSSVETNIGNPFDMVTRFGAPVSGVYFFTFSMKHEDVEEYVYLMHNGMT 188
 DB 563 PAYGAPIDPFDELLYNRQOHYDPRSGITFKIKPIGYFYSYHV--HYKGTTHVWGLYKNGTP 620

QY 189 VFSWSTYE--MKGKSDTSSNHAIVLKLAKGDEVWLMGN---GALGDRHORESTFAGFL 242
 DB 621 --TMTYDEYSKGYLDQASGSAIMELTENDQVWLQLPNAESNGLYSSEYVHSSFGFLV 677

RESULT 12
 CA1A_BOVIN STANDARD: PRT: 674 AA.
 AC P23206;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Collagen alpha 1(X) chain precursor.
 GN COL10A1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=9113131; PubMed=1703407;
 RA Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
 RT "Isolation of cDNAs encoding the complete sequence of bovine type X
 collagen. Evidence for the condensed nature of mammalian type X
 collagen genes.";
 RL Biochem. J. 273:141-148(1991).
 CC -I- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
 CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
 CC MINERALIZATION ZONES OF HALINE CARTILAGE.
 CC -I- SUBUNIT: HOMOTRIMER.
 CC -I- PPM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -I- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
 CC -I- SIMILARITY: CONTAINS 1 C10 DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X53556; CAA37624.1; -
 CC PIR: S13301; S13301.
 CC InterPro: IPR001073; C1g.
 CC InterPro: IPR000087; Collagen.
 CC Pfam: PF00386; C1g; 1.

DR Pfam: PF01391; Collagen: 9.
 DR PRINTS: PR00007; COMPLEMENTC1Q.
 DR ProDom: PD000007; Collagen: 1.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS01113; C1Q; 1.
 KW Extracellular matrix; connective tissue; Repeat; Hydroxylation;
 KW Cartilage; Collagen; Signal; Glycoprotein.
 FT SIGNAL 1 18
 FT CHAIN 19 674 COLLAGEN ALPHA 1(X) CHAIN.
 FT DOMAIN 19 56 NONHELICAL REGION (NC2).
 FT DOMAIN 57 519 TRIPLE-HELICAL REGION.
 FT DOMAIN 520 674 NONHELICAL REGION (NC1).
 FT DOMAIN 539 674 C1Q.
 FT DISULFID 194 197 BY SIMILARITY.
 FT MOD_RES 460 460 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 463 463 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC, C) (POTENTIAL).
 SO SEQUENCE 674 AA: 65346 MW: CDACAT3A03E004CA CRC64:

Query Match 20.1%; Score 275; DB 1; Length 674;
 Best Local Similarity 30.0%; Pred. No. 8e-16;
 Matches 72; Conservative 31; Mismatches 87; Indels 50; Gaps 6;

QY 51 GYQGPFGPPGPPGPGPGIPGNGHNGNNGATGHEGAKGKGD-----KDLGPRGEG 99
 DB 434 GNGEAGRGPGVGPICPTGRPIGPPGPGSGKGDVGTGPPGPGIAYKVGNGPTGPG 493
 QY 100 QHGPKEGKGPICP-----PELQIA-----FMASLATHFSNONGII----- 136
 DB 494 PPGPGNMGEPGLPPGPPGPPGGOVALPDEPVKAGORPFSVANGVGMPYSATFVILS 553
 QY 137 -----FSSVETNIGNPFDMVTRFGAPVSGVYFFTFSMKHEDVEEYVYLMH 185
 DB 554 KAYPAIGPIPDKILYKNQOHYDPTGTGIFCKIPGIYFYSYHI--HYKGTTHVWGLYK 611

QY 186 GNTVFSMTSYEMKKSDDTSSNHAIVLKLAKGDEVWLM---GNGALGDRHORESTFAGFL 242
 DB 612 GTPVMTYDEYIKGYLDQASGSAVIDLTENDQVWLQLPNAGSNGLYSPREYHSSFGFLV 671

RESULT 13
 C1QC_MOUSE STANDARD: PRT: 246 AA.
 ID C1QC_MOUSE
 AC 002105;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Complement C1q subcomponent, C chain precursor.
 GN C1Q OR C1QC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RX MEDLINE=9301118; PubMed=1396691;
 RA Petry F., Reid K.B.M., Loos M.;
 RT "Isolation, sequence analysis and characterization of cDNA clones
 RT coding for the C chain of mouse C1q. Sequence similarity of
 RT complement subcomponent C1q, collagen type VIII and type X and
 RT precerebellin.";
 RL Eur. J. Biochem. 209:129-134(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=96186528; PubMed=8606057;
 RA Petry F., McClive P.J., Botta M., Morley B.J., Morahan G., Loos M.;
 RT "The mouse C1q gene associates with the PROENZYME C1R AND C1S TO YIELD
 RT conservation of gene organization.";
 RL Immunogenetics 43:370-376(1996).
 CC -I- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYME C1R AND C1S TO YIELD
 CC C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE

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OM protein - protein search, using sw model

Run on: January 15, 2003, 19:32:00 ; Search time 91 Seconds
(without alignments)
557.006 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MIMROLIYWOLALFLPLFC.....LHGDHQRSTFAGFLPFTK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1311	95.9	246	11	Q9ES30 mus musculu
2	313	22.9	294	11	Q9D804
3	299	21.9	240	6	Q95M04
4	293.5	21.5	243	6	Q95J07
5	276.5	20.2	675	6	Q9N178
6	273	20.0	1077	4	Q8RE71
7	270	19.8	295	11	Q9Z1K4
8	266.5	19.5	158	4	Q9H67
9	258.5	18.9	705	4	Q8REJ5
10	257.5	18.8	243	11	Q8R002
11	257.5	18.8	744	4	Q9ED07
12	257	18.8	744	11	Q9D2V4
13	257	18.8	744	11	Q921S8
14	247.5	18.1	194	6	Q9S395
15	239.5	17.5	245	11	Q9DCM6
16	237.5	17.4	281	11	Q9QXP7

17	219.5	16.1	347	4	Q961H6	Q961H6 homo sapien
18	218	15.9	1017	11	Q99K41	Q99K41 mus musculu
19	216	15.8	2944	11	Q63870	Q63870 mus musculu
20	215	15.7	583	4	Q96G58	Q96G58 homo sapien
21	215	15.7	992	4	Q9UC76	Q9UC76 homo sapien
22	215	15.7	1016	4	Q9YEC2	Q9YEC2 homo sapien
23	211	15.4	182	11	Q8RI2	Q8RI2 mus musculu
24	210.5	15.4	422	5	Q24893	Q24893 ephydactia m
25	207.5	15.2	1549	11	Q60444	Q60444 cricetus
26	203.5	14.9	673	4	Q14052	Q14052 homo sapien
27	197	14.4	171	13	Q90586	Q90586 gallus galli
28	195.5	14.3	1140	11	Q61434	Q61434 mus musculu
29	195.5	14.3	1774	11	Q62001	Q62001 mus musculu
30	194	14.2	224	5	Q9VYV2	Q9VYV2 drosophila
31	194	14.2	397	16	Q8X1T5	Q8X1T5 clostridium
32	191.5	14.0	294	5	Q9VEP4	Q9VEP4 drosophila
33	190.5	13.9	289	5	Q62432	Q62432 caenorhabd
34	190.5	13.9	890	5	Q77087	Q77087 alvinella p
35	190	13.9	476	13	Q918D5	Q918D5 gallus galli
36	189	13.8	292	11	Q9CSB7	Q9CSB7 mus musculu
37	189	13.8	375	4	Q8TCD8	Q8TCD8 homo sapien
38	188.5	13.8	187	11	Q9JHA9	Q9JHA9 rattus norv
39	188.5	13.8	1745	4	Q9NZ06	Q9NZ06 homo sapien
40	188	13.8	1344	13	Q93419	Q93419 gallus galli
41	187.5	13.7	680	11	Q9D0D2	Q9D0D2 mus musculu
42	185.5	13.6	303	5	Q23364	Q23364 caenorhabd
43	185.5	13.6	1723	5	Q9GGB1	Q9GGB1 hydra atten
44	185	13.5	408	13	Q90604	Q90604 gallus galli
45	185	13.5	441	4	Q96A84	Q96A84 homo sapien

ALIGNMENTS

RESULT 1	Q9ES30	PRELIMINARY:	PRT:	246 AA.
ID	Q9ES30			
AC	Q9ES30			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Collagenous repeat-containing sequence of 26kDa protein.			
GN	CORS OR CORS26.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxId=10990;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-21264842; PubMed-11071891;			
RA	Maeda T., Abe M., Kurisu K., Jikko A., Furukawa S.;			
RT	"Molecular cloning and characterization of a novel gene, CORS26,			
RT	encoding a putative secretory protein and its possible involvement in			
RT	skeletal development."			
RL	J. Biol. Chem. 276:3628-3634 (2001).			
DR	EMBL; AF246265; AAG33704.1; .			
DR	MCD; MGT:1932136; Cors.			
DR	InterPro; IPR001073; C1q.			
DR	InterPro; IPR000087; Collagen.			
DR	Pfam; PF00386; C1q; 1.			
DR	Pfam; PF01391; Collagen; 1.			
DR	PRINTS; PR00007; COMPLEMENTC1Q.			
DR	SMART; SM00110; C1Q; 1.			
DR	PROSITE; PS01113; C1Q; 1.			
DR	SEQUENCE 246 AA; 26828 MW; 42A481B3E9F48F7E CRC64;			
QY	1 MIMROLIYWOLALFLPLFCODEYNESQGTGSLPPDCCKCHGDSYFSGYGPPEPPG 60			
DB	1 MIMROLIYWOLALFLPLFCODEYNESQGTGSLPPDCCKCHGDSYFSGYGPPEPPG 60			
	Best local similarity 95.9%; Score 1311; DB 11; Length 246;			
	Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps 0;			


```

QY 61 PGCTGNHNGNNGATGHEGAKGKDGKDLGPRGRCGQHPKCKGPGIPELOIAF 120
DB 61 PPGCTGNHNGNNGATGHEGAKGKDGKDLGPRGRCGQHPKCKGPGIPELOIAF 120
QY 121 MASLATHFNSQNGIIFSSVETNIGNFEDVMTGRGAPVSGVYFFTFSSMKHEDVEEYV 180
DB 121 MASLATHFNSQNGIIFSSVETNIGNFEDVMTGRGAPVSGVYFFTFSSMKHEDVEEYV 180
QY 181 YLMHNGNTVFSYSTEEMKKSQDTSNNHAYLKLAKGDEWLMRGNGALHGHORESTFAGE 240
DB 181 YLMHNGNTVFSYSTEEMKKSQDTSNNHAYLKLAKGDEWLMRGNGALHGHORESTFAGE 240
QY 241 LLEFETK 246
DB 241 LLEFETK 246

RESULT 2
QY 09DBU4 PRELIMINARY: PRT: 294 AA.
AC 09DBU4
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1810033K05RIK protein.
CN 1810033K05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shiragawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Araiwa T., Hara A., Fukunishi Y., Kono H., Aachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK007683; BAB25187.1; -
DR MGI: MGI:1916433; 1810033K05RIK.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 2.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
SQ SEQUENCE 294 AA; 30865 MW; 6D3905AE7C19B6FA CRC64;

Query Match 22.9%; Score 313; DB 11; Length 294;
Best Local Similarity 28.9%; Pred. No. 3.8e-20;
Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;
QY 6 LLYWOLIAFLPFCICODEYM-----ESPQTGLPPDCSKCHQDSFRGCGPPGP 59
DB 10 MTSWVLLAC-ALP---CAADPMLGAFARRDPKGGPQLVCS-----LPGGCGPP 54

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QY 60 GPPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGRCGQHPKCKGPGIPELOIAF 120
DB 55 GPPGAPGSSGVVGRMRGPFCKDQDQDGDGRGSGEBGPPGRTGNKCKGPKKACAGCA 114
QY 93 GPRGER-----GQHPKCKGKGYGPI-----PELOIAFMASLATHFNSQNS 133
DB 115 GPRGKGVSGTCKHGTGKPKCKGKGPGLPGCSCSSRAKSAFSAVAVKSYREKL 174
QY 134 GTFSSVETNIGNFEDVMTGRGAPVSGVYFFTFSSMKHEDVEEYVYLMHNGNTVF 190
DB 175 PIKFKIILMEGHNASGKFEVCSVPGIYFTYDITLANKH-----LAIGLVHNGO--Y 227
QY 191 SMYSYEMK-GKSDTSNNHAYLKLAKGDEWLMR-----GNGLAHGHORESTFAGE 243
DB 228 RIRFDANTGNHNVASGSTTLALKEGDEWLMR-----LAIGLVHNGO--Y 227

RESULT 3
QY 095MQ4 PRELIMINARY: PRT: 240 AA.
AC 095MQ4
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adipose tissue-specific protein adipo Q.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21369933; PubMed=11382781;
RA Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;
RT "Identification and Adipocyte Differentiation-dependent Expression of
RT the Unique Distal Acid Residue in an Adipose Tissue-specific
RT Glycoprotein, Adipo Q."
RL J. Biol. Chem. 276:28849-28856(2001).
DR EMBL: AF269230; AAK58902.1; -
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 1.
DR ProDom: PD000007; Collagen; 1.
DR PROSITE: PS01113; C1Q; UNKNOWN; 1.
SQ SEQUENCE 240 AA; 26091 MW; C6253BA803B9A668 CRC64;

Query Match 21.9%; Score 289; DB 6; Length 240;
Best Local Similarity 33.3%; Pred. No. 5.4e-19;
Matches 75; Conservative 35; Mismatches 85; Indels 30; Gaps 7;
QY 44 HGDYSEFRGYGPPGPPG-----PGIPGNHNGNNGATGHEGAKGKDGKDLGPR 95
DB 16 HGEDNM---EDPPLPKGACAGMAGIPGPHNGTPGRGRGRTGPEKCKGKDGAGLLGR 72
QY 96 GER---GQHPKCKGKGYGPIPE-----LQIAFMASLATHFNSQNSGTFSSVET 142
DB 73 GETGDVMTGAGCPGPFPTPKRKEPGEAAYVYSASFVSGLETRVYVNVDIRFKIEY 132
QY 143 NTFGNFEDVMTGRGAPVSGVYFFTFSSMKHEDVEEYVYLMHNGNTVFSYSEMKKSD 202
DB 133 NOQNHFDGSGTKFYCNIPLYFTYHITYY--MKDVKSLEFKKRAVLFTYDQYOEKNVD 190
QY 203 TSSNHAYLKLAKGDEWLMRGNGALH-----GNHORESTFAGEFLF 243
DB 191 QASGSVLLHLEVDQVWLVQVYEGENHNGYADVNDSTFTGFLY 235

RESULT 4
QY 095JDT PRELIMINARY: PRT: 243 AA.
AC 095JDT

```


RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Cuslinsich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT *Functional annotation of a full-length mouse cDNA collection.*
 RL Nature 409:685-690(2001).
 DR EMBL: AK018742; BAB31383.1; -
 DR MGD: MGI:88463; Col8a1.
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; C1q; 1.
 DR Pfam: PF01391; Collagen; 7.
 DR PRINTS: PR00007; COMPLEMENTC1Q.
 DR SMART: SM00110; C1Q; 1.
 DR PROSITE: PS01113; C1Q; 1.
 SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCD6EB9C CRC64;

Query Match 18.8%; Score 257; DB 11; Length 744;
 Best Local Similarity 29.6%; Pred. No. 1.2e-14;
 Matches 77; Conservative 27; Mismatches 102; Indels 54; Gaps 6;

OY 34 GLPPDCCKCHGDIYFSGYOGPPPPGPIPGHNGNNGATGCHGA-----KGE 85
 DB 487 GIPGD--QGLOGPPGIGIVGPPGIPGIPGKGGGLGPPGPGVGRVAGLHGP 544
 OY 86 KGDKGDLGPPRGEGOHGPKGKGYPCIP-----PELQI-----118
 DB 545 PGKRGALGPGQGPPLPPPPGPPGPPPAVMPPTSPGGEYLPDMGLGIDGVKPPHAYAGK 604
 OY 119 -----AFMASLATHFSNONGIIFSSVETNIGNEFDVWTRFGAPVSGVYEFT 166
 DB 605 KGRKGPAVEPAFTALTEVPPVPGAPVKDKLLYNQRQNYNQTGIFICEVGVYFA 664
 OY 167 FSNMKHEDVEEVYVYLHNGTIVFSMYSEKKGSDTSSNNAVLKLAGDEVLMRGN-- 224
 DB 665 YHV--HCKGNVWVALFKNNPEPMYTYDEYKKGFLDQASGSAVILLRPGDQVFLQMPSEQ 722
 OY 225 -GALHGDHORESTFAGFLF 243
 DB 723 AAGLYAGQVHSSSTGYLLY 742

RESULT 13

0921S8 PRELIMINARY; PRT; 744 AA.
 AC 0921S8;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Procollagen, type VIII, alpha 1.
 GN COL8A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011061; AAH1061.1; -
 DR MGD: MGI:88463; Col8a1.
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; C1q; 1.
 DR Pfam: PF01391; Collagen; 7.
 DR PROSITE: PS01113; C1Q; UNKNOWN_1.
 KW Collagen.
 SQ SEQUENCE 744 AA; 73621 MW; BF7A7ED79D8463AA CRC64;

Query Match 18.8%; Score 257; DB 11; Length 744;
 Best Local Similarity 29.6%; Pred. No. 1.2e-14;
 Matches 77; Conservative 27; Mismatches 102; Indels 54; Gaps 6;
 OY 34 GLPPDCCKCHGDIYFSGYOGPPPPGPIPGHNGNNGATGCHGA-----KGE 85
 DB 487 GIPGD--QGLOGPPGIGIVGPPGIPGIPGKGGGLGPPGPGVGRVAGLHGP 544
 OY 86 KGDKGDLGPPRGEGOHGPKGKGYPCIP-----PELQI-----118
 DB 545 PGKRGALGPGQGPPLPPPPGPPGPPPAVMPPTSPGGEYLPDMGLGIDGVKPPHAYAGK 604
 OY 119 -----AFMASLATHFSNONGIIFSSVETNIGNEFDVWTRFGAPVSGVYEFT 166
 DB 605 KGRKGPAVEPAFTALTEVPPVPGAPVKDKLLYNQRQNYNQTGIFICEVGVYFA 664
 OY 167 FSNMKHEDVEEVYVYLHNGTIVFSMYSEKKGSDTSSNNAVLKLAGDEVLMRGN-- 224
 DB 665 YHV--HCKGNVWVALFKNNPEPMYTYDEYKKGFLDQASGSAVILLRPGDQVFLQMPSEQ 722
 OY 225 -GALHGDHORESTFAGFLF 243
 DB 723 AAGLYAGQVHSSSTGYLLY 742

RESULT 14

095J95 PRELIMINARY; PRT; 194 AA.
 AC 095J95;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Adiponectin (Fragment).
 GN APM1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADIPOSE TISSUE;
 RA Kabir M., Anantharayan S., Ionut V., Kim S.P., Van Citters G.W.,
 RA Des M.K., Bergman R.N.;
 RT "Regulation of Adiponectin gene expression in the fat-fed dog."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF417206; AAL09702.1; -
 DR InterPro: IPR001073; C1q.
 DR InterPro: IPR000087; Collagen.
 DR Pfam: PF00386; C1q; 1.
 DR Pfam: PF01391; Collagen; 1.
 DR ProDom: PD000007; Collagen; 1.
 DR PROSITE: PS01113; C1Q; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 194 194
 SQ SEQUENCE 194 AA; 20890 MW; 3AA3D947D187AF9A CRC64;

Query Match 18.1%; Score 247.5; DB 6; Length 194;
 Best Local Similarity 30.9%; Pred. No. 1.7e-14;
 Matches 60; Conservative 36; Mismatches 71; Indels 27; Gaps 6;

OY 54 GP-----PGPPGP-----GIPGNHGNNGNNGATGHEGAKGEGDKGD--LGPGRGQ- 100
 DB 1 GPGVLLPLPKGACPGCMAGIPGHPGHNTPGHDGKGDTFGEKGGDGLVPGKDDTGET 60
 OY 101 --HGPKGEGYGPPIPEL-----QIAFMASLATHFSNONGIIFSSVETNIGNEF 148
 DB 61 GVTGVEGPRGPGTGRGGEPSAVYHRSAPSVGLSERTIVPVPPIRTKLFYNLQNH 120
 OY 149 DVWTRFGAPVSGVYEFTFSNMKHEDVEEVYVYLHNGTIVFSMYSEKKGSDTSSNHA 208
 DB 121 DGTGKFGHCNIPGLVYFSYHITVY--LKDVKVSLYKKDKAMLETYDQYQEKHVDQASGV 178
 OY 209 VLKLAKGDEVLMR 222

Db 179 LHLLEVGQVWLVQ 192

RESULT 15

09DCM6 PRELIMINARY; PRT: 245 AA.

AC 09DCM6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Complement component 1, q subcomponent, alpha polypeptide.
GN C1QA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]

RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK002655; BAB2262.1; -;
DR EMBL: BC002086; AA02086.1; -;
DR MGI: 88223; C1qa.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 1.
DR PRINTS: PRO0007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
SQ SEQUENCE 245 AA; 25974 MW; 41C2066D49592020 CRC64;

Query Match 17.5%; Score 239.5; DB 11; Length 245;
Best Local Similarity 33.2%; Pred. No. 1.2e-13;
Matches 71; Conservative 26; Mismatches 94; Indels 23; Gaps 7;

QY 51 GYGGPPGPPGPGIPGNHNGNNGATG-HEGAKGEKDKGD-----LGP 94
DB 31 GKGAGPENGPRGPRGLKGERGEGAGIRGTGIRGFGDPGESGPRGPNVGLRPSGP 90
QY 95 RGERGQHGRKGEKYPG-IPPELOIAFMASLATHFSNONGSIIFSSVETNIGNFPDWTG 153
DB 91 LGDSGPGGLKGVGNPNINRQPRAPSAIFRONPMTLGNV-VIPDKVLTFOESPYQNHG 149
QY 154 RFGAPVGVGVFEFTFSMKHEDVEVYVYLMHNG--NTVFSMYSTEMKCKSDTSSNHAFLK 211
DB 150 RFTCAVGVGFYFNFQVTSKMDL-CLFTKSSSGGQPRDLSFSNTNKGFLFOVLAGTVLQ 208

OY 212 LAKGDEWVLRM--GNGALHGDHQRSTFAGFLIF 243
DB 209 LRRGDEWVIERKDPKRGRIYQGTEDSIFSGFLIF 242

Search completed: January 15, 2003, 19:39:47
Job time : 94 secs

GenCore version 5.1.3
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OH protein - protein search, using sw model

Run on: January 15, 2003, 19:37:15 ; Search time 244 Seconds
(without alignments)
20.041 Million cell updates/sec

Title: US-10-036-041-2

Perfect score: 1367

Sequence: 1 MLMQLIYMWLLALFLPFC.....LHGDRHFRSTFAGLLFETK 246

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCIT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1367	100.0	246	9	US-10-036-041-2
2	1367	100.0	246	9	US-10-035-855-2
3	1367	100.0	246	12	US-10-036-342-2
4	294	21.5	247	10	US-09-776-976-4
5	294	21.5	247	10	US-09-758-055-4
6	294	21.5	247	10	US-09-909-547-4
7	293.5	21.5	244	10	US-09-911-176B-8
8	293.5	21.5	244	10	US-09-776-976-6
9	293.5	21.5	244	10	US-09-758-055-6
10	293.5	21.5	244	10	US-09-909-547-6
11	293	21.4	247	10	US-09-776-976-2
12	293	21.4	247	10	US-09-758-055-2
13	293	21.4	247	10	US-09-909-547-2
14	290.5	21.3	259	9	US-09-992-598-47
15	290.5	21.3	259	9	US-09-988-293A-47
16	290.5	21.3	259	9	US-09-988-735-47
17	290.5	21.3	259	9	US-09-990-444-47
18	290.5	21.3	259	9	US-09-989-730-47
19	290.5	21.3	259	9	US-09-990-436-47

20	290.5	21.3	259	9	US-09-991-181-47	Sequence 47, Appl
21	290.5	21.3	259	9	US-09-993-687-47	Sequence 47, Appl
22	290.5	21.3	259	9	US-09-989-734-47	Sequence 47, Appl
23	290.5	21.3	259	9	US-09-997-653-47	Sequence 47, Appl
24	290.5	21.3	259	9	US-10-174-590-62	Sequence 62, Appl
25	290.5	21.3	259	9	US-10-176-758-62	Sequence 62, Appl
26	290.5	21.3	259	10	US-09-989-722-47	Sequence 47, Appl
27	290.5	21.3	259	10	US-09-989-723-47	Sequence 47, Appl
28	290.5	21.3	259	10	US-09-989-727-47	Sequence 47, Appl
29	290.5	21.3	259	10	US-09-989-731-47	Sequence 47, Appl
30	290.5	21.3	259	10	US-09-989-732-47	Sequence 47, Appl
31	290.5	21.3	259	10	US-09-991-073-47	Sequence 47, Appl
32	290.5	21.3	259	10	US-09-990-442-47	Sequence 47, Appl
33	290.5	21.3	259	10	US-09-991-163-47	Sequence 47, Appl
34	290.5	21.3	259	10	US-09-993-604-47	Sequence 47, Appl
35	290.5	21.3	259	10	US-09-990-456-47	Sequence 47, Appl
36	290.5	21.3	259	10	US-09-989-721-47	Sequence 47, Appl
37	290.5	21.3	259	12	US-10-052-586-62	Sequence 62, Appl
38	290.5	21.3	278	10	US-09-799-777-35	Sequence 35, Appl
39	289.5	21.2	247	9	US-09-911-176B-3	Sequence 3, Appl
40	287	21.0	746	9	US-09-854-133-185	Sequence 185, App
41	273	20.0	746	10	US-09-738-973-185	Sequence 185, App
42	264.5	19.3	243	9	US-09-944-403-42	Sequence 42, Appl
43	264.5	19.3	243	9	US-09-944-403-42	Sequence 42, Appl
44	264.5	19.3	243	9	US-09-944-403-42	Sequence 42, Appl
45	264.5	19.3	243	9	US-09-944-896-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-036-041-2
Sequence 2, Application US/10036041
Publication No. US2002019251A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C8
CURRENT APPLICATION NUMBER: US/10/036, 041
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: 60/125826
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/127035
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/127706
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/129122
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/130359
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131272
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138166
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 09/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
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PRIOR FILING DATE: 2000-08-23
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PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956

PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Homo Sapien
US-10-036-041-2
Query Match 100.0%; Score 1367; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 9,9e-112;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 MUMRQLIYWQLALFLPFLCICQDEYNESPQTGGLPPDCSKCHGDSYFRGCGPPGPG 60
DB 1 MUMRQLIYWQLALFLPFLCICQDEYNESPQTGGLPPDCSKCHGDSYFRGCGPPGPG 60
QY 61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKEGYPCIPPELQIAF 120
61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKEGYPCIPPELQIAF 120
DB 121 MASLATHPSNONGSLIFSSVETNIGNEFDWTRGFGAPVSGVYFEFTSMKHDEVEEYV 180
121 MASLATHPSNONGSLIFSSVETNIGNEFDWTRGFGAPVSGVYFEFTSMKHDEVEEYV 180
QY 181 YLMHNGTVFSMYSYEKKGSDTSSNHAIVLKLAKGDEWLMRGALHGHORESTFAGF 240
181 YLMHNGTVFSMYSYEKKGSDTSSNHAIVLKLAKGDEWLMRGALHGHORESTFAGF 240
DB 181 YLMHNGTVFSMYSYEKKGSDTSSNHAIVLKLAKGDEWLMRGALHGHORESTFAGF 240
QY 241 LLEETK 246
241 LLEETK 246
DB 241 LLEETK 246
241 LLEETK 246
RESULT 2
US-10-035-855-2
Sequence 2, Application US/10035855
Publication No. US20030008348A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030RIC4
CURRENT APPLICATION NUMBER: US/10/035,855
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
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PRIOR FILING DATE: 1999-03-23
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PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/127035
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PRIOR APPLICATION NUMBER: 60/127706
PRIOR FILING DATE: 1999-04-05
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PRIOR FILING DATE: 1999-05-04
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PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: 60/135750
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PRIOR FILING DATE: 1999-06-08
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PRIOR APPLICATION NUMBER: 60/146970
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PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/644848
PRIOR FILING DATE: 2000-08-22
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PRIOR FILING DATE: 2000-12-20
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PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908.827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10733
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
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PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
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PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Homo Sapien
US-10-035-855-2

Query Match 100.0%; Score 1367; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. 9.9e-112;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIMROLIYWQALLAFELPPLCQDEYMESPOTGCLPPDCSKCHDYSRGYPGPPPG 60
Db 1 MIMROLIYWQALLAFELPPLCQDEYMESPOTGCLPPDCSKCHDYSRGYPGPPPG 60
Qy 61 PPGIGNNGNNGNNGATGHEGAKGEGDKGDLGPRGERGOGHPKGEKGPGLPELOIAF 120
Db 61 PPGIGNNGNNGNNGATGHEGAKGEGDKGDLGPRGERGOGHPKGEKGPGLPELOIAF 120
Qy 121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRFAGVSGVYFFTFSMKHEDVEEYV 180
Db 121 MASLATHFSNONGIIFSSVETNIGNFDVMTGRFAGVSGVYFFTFSMKHEDVEEYV 180
Qy 181 YLMHNGNTVFSWYSYEMKGSPTSNNHVLKIAKGDEYWLRMGNGALHGDHORESTFAGF 240
Db 181 YLMHNGNTVFSWYSYEMKGSPTSNNHVLKIAKGDEYWLRMGNGALHGDHORESTFAGF 240
Qy 241 LLEFETK 246
Db 241 LLEFETK 246

RESULT 3
US-10-036-342-2
Sequence 2, Application US/10036342
Patent No. US2002090681A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C5

;; CURRENT APPLICATION NUMBER: US/10/036,342
;; CURRENT FILING DATE: 2001-12-26
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/112514
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;; PRIOR FILING DATE: 2001-06-29
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;; PRIOR APPLICATION NUMBER: PCT/US99/10733
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;; PRIOR APPLICATION NUMBER: PCT/US99/28551
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;; PRIOR APPLICATION NUMBER: PCT/US00/05601
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;; PRIOR APPLICATION NUMBER: PCT/US00/34956
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 80
;; SEQ ID NO 2
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo Sapien
;; US-10-036-342-2

Query Match 100.0%; Score 1367; DB 12; Length 246;
Best Local Similarity 100.0%; Pred. No. 9,9e-112;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMROLIYQMLALFFLPFCICODEYMS.POTGGLPPCCKCHGDYSFRGYPGPG 60
Db 1 MLMROLIYQMLALFFLPFCICODEYMS.POTGGLPPCCKCHGDYSFRGYPGPG 60
QY 61 PPGIPGNHGNNGNNGATGHEGAKGEGDKGDLGPRGERGQHPKGEKGYPGIPPELQIAF 120
Db 61 PPGIPGNHGNNGNNGATGHEGAKGEGDKGDLGPRGERGQHPKGEKGYPGIPPELQIAF 120
QY 121 MASLATHFSNONSGLITSSVETNIGNFEDVVTGRFGAFAVSVYFFTESMMKHEDVEEYV 180
Db 121 MASLATHFSNONSGLITSSVETNIGNFEDVVTGRFGAFAVSVYFFTESMMKHEDVEEYV 180
QY 181 YLMHNGTVFSMTSEYKKGKSDTSSNHAVALKLAKGDEVYLMGNGALHGDHORESTFAGF 240
Db 181 YLMHNGTVFSMTSEYKKGKSDTSSNHAVALKLAKGDEVYLMGNGALHGDHORESTFAGF 240
QY 241 LLEFETK 246
Db 241 LLEFETK 246

RESULT 4
US-09-776-976-4
; Sequence 4, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Finebis, Joachim

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: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76, US4, REG.
: CURRENT APPLICATION NUMBER: US/09/776, 976
: CURRENT FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: US 09/758, 055
: PRIOR FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/176, 228
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/198, 087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/299, 881
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 4
: LENGTH: 247
: TYPE: PRT
: ORGANISM: mus musculus
US-09-776-976-4

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Query Match      21.5%  Score 294;  DB 10;  Length 247;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

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DB 2 LLLQALLFLILLP-SHAEDVYTTTELAPALVPPKGTCA-----GMA-----GIPG 48
OY 64 IPGNHNGNNGCATGHEGAKGKGDGLGPRGER---GQHPKGEKGYPGIPE----- 115
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 49 HPGHNGTPEGDRDGTGPKGKGDAGLLGPKGETGDMTGAEGRGPGTGRKGEPC 108
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 116 -----LQIAFMA5LATHEFNSNGIIFSSVETNIGNFPDVMTRGRCAPVSGVYFTFSM 170
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DB 109 EAAVYR5AF5VGLERIVYVNPVPIRFTKIFYNQONHVDG5TGKFCNIPGLYFSYHIT 168
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OY 227 LKHGHORFSTFAGFLIF 243
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RESULT 5
US-09-758-055-4
: Sequence 4, Application US/09758055
: Patent No. US20020058617A1
: GENERAL INFORMATION:
: APPLICANT: Fruebis, Joachim
: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76, US4, REG.
: CURRENT APPLICATION NUMBER: US/09/758, 055
: CURRENT FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/176, 228
: PRIOR FILING DATE: 2000-01-14
: PRIOR APPLICATION NUMBER: US 60/198, 087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/299, 881
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 4
: LENGTH: 247
: TYPE: PRT
: ORGANISM: mus musculus

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US-09-758-055-4

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Query Match      21.5%  Score 294;  DB 10;  Length 247;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

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OY 6 LLYWOLALFFLPCLCODEYVESPOTG--LPPDCSKCHGDYSFRGYQGPFGPPG 63
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DB 2 LLLQALLFLILLP-SHAEDVYTTTELAPALVPPKGTCA-----GMA-----GIPG 48
OY 64 IPGNHNGNNGCATGHEGAKGKGDGLGPRGER---GQHPKGEKGYPGIPE----- 115
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 49 HPGHNGTPEGDRDGTGPKGKGDAGLLGPKGETGDMTGAEGRGPGTGRKGEPC 108
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 116 -----LQIAFMA5LATHEFNSNGIIFSSVETNIGNFPDVMTRGRCAPVSGVYFTFSM 170
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 109 EAAVYR5AF5VGLERIVYVNPVPIRFTKIFYNQONHVDG5TGKFCNIPGLYFSYHIT 168
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OY 171 KHEDEEYVYVLMHNGNTVFSMYSTEMKGSJDTSSNHAVLKLAKGDEWLRM-GNG---A 226
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 169 VY--MKDVKVSLEFKDKAVLFTYDQYQEKNVQASGSVLLHLEVGDQWLQYVGDDHNG 226
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OY 227 LKHGHORFSTFAGFLIF 243
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 227 LYADVNDSTFTGFLY 243
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RESULT 6
US-09-909-547-4
: Sequence 4, Application US/09909547
: Patent No. US20020091080A1
: GENERAL INFORMATION:
: APPLICANT: Fruebis, Joachim
: APPLICANT: Erickson, Mary Ruth
: APPLICANT: Yen, Frances
: TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
: FILE REFERENCE: 76, US6, CIP
: CURRENT APPLICATION NUMBER: US/09/909, 547
: CURRENT FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: US 09/776, 976
: PRIOR FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: US 09/758, 055
: PRIOR FILING DATE: 2001-01-10
: PRIOR APPLICATION NUMBER: US 60/299, 881
: PRIOR FILING DATE: 2000-09-01
: PRIOR APPLICATION NUMBER: US 60/198, 087
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: US 60/176, 228
: PRIOR FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patent.pm
: SEQ ID NO 4
: LENGTH: 247
: TYPE: PRT
: ORGANISM: mus musculus
US-09-909-547-4
Query Match      21.5%  Score 294;  DB 10;  Length 247;
Best Local Similarity 31.5%; Pred. No. 1.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

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QY 208 AVLKLAKGDEWVLRM-GNG---ALHGHQRFSTPAFLLE 243
      :| | |||::| | |::| | |||:
Db 201 VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGLLY 240

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RESULT 10
US-09-909-547-6
; Sequence 6, Application US/09909547
; Patent No. US20020001080A1

```

; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT:

```

TITLE OF INVENTION: OB3G Globular Head and Uses Thereof for Decreasing Body Mass

FILE REFERENCE: 76.Us6.CIP

CURRENT APPLICATION NUMBER: US/09/909,547

CURRENT FITTING NUMBER: 300.0210

Query Match	21.5%;	Score 293.5;	DB 10;	Length 244;
Best Local Similarity	34.5%;	Pred. No. 1.7e-18;		
Matches 76; Conservative	35;	Mismatches 78;	Indels 31;	Gaps 9;

QY 98 RGQHGPRGCKEYPCG-----PPE-----LQIAFMASLATHFSNONGSIITSSVETNIGNF 147
 | | : | : | | | | : | | : | | : | |
 Db 83 TGVPGAEPRGPRGPIQGRKCEPGEGAVVYRSASFVGLLEYVTIPNMPPIRFYKIFYNQNH 1422

QY 148 EDVMTGREGAPVSQVFETFSMKHDEVEEVLVYLIMHGNTVESMYSYEKKGKSDTSSNH 2077
: : | | : : | : : : : : : : : : :
Db 143 YDGTGFHCNIPGLFYFAHYHTVV--MKDVKSLSFKDKAMLEFTYDQIQENNVDASGS 2000

QY 208 AVLKAKAGDEWLRM-GNG---ALGHQHQRFTSFAGFLTF 243
:
Db 201 VLHLEFVGDDQWLQVYGEGERNGLADNDNDSTFTGFLYL 240

RESULT 11
US-09-776-976-2
; Sequence 2, Application US/09776976
; Patent No. US20020037849A1

APPLICANT: Fruebis, Joachim
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances

TITLE OF INVENTION: OBG3 Globalular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.054.REG
CURRENT APPLICATION NUMBER: US/09/776,976

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US-09-776-976--2
?
? ORGANISM: mus musculus
?
? LENGTH: 247
? TYPE: PRT
? SOFTWARE: Patent.pm
? SEQ ID NO 2
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? PRIOR FILING DATE: 2000-01-14
? PRIOR APPLICATION NUMBER: US 60/176,228
? PRIOR FILING DATE: 2000-04-13
? PRIOR APPLICATION NUMBER: US 60/299,881
? PRIOR FILING DATE: 2000-09-01
? NUMBER OF SEQ ID NOS: 7
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? SOFTWARE: Patent.pm
? SEQ ID NO 2
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? LENGTH: 247
? TYPE: PRT
? ORGANISM: mus musculus
?
? US-09-776-976--2
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Query Match	21.4%	Score 293;	DB 10;	Length 247;
Best Local Similarity	31.2%	Pred. No. 1.9e-18;		
Matches 81, Conservative	40;	Mismatches 99;	Indels 40;	Gaps 10;

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QY      64 IPENHGNNNGATGHEGAKGEKGD--LGRGER---GQHPKGEKGYRGTPE-- 115
      ||| :||| | : : ||||:|||| |||:| | : : :||| |
DQ      46 IPENHGNNSTPRGDRGDRGTPEGEKEKGDGCLLPKGETGDVGMGAEGPRGPTGRKG 105

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QY      116 -----LQIAFMASLATIHFSNONGIIFSSVETNICGFEDVTGRFGAPVSGVIFFTF 167  
          : | | : | | : | | : | | : | | :  
Db      106 EPGEAAYYYRSGFVGLETRTVTPNPPIRFRTKIFYNQNHYNSTGKFYCINPGLTYFSY 165
```

DQ 168 SNAKHEDVEEYVYLHMGNTVFMSIYEEMKCKSDTSSHHAVLKLAKGDVEWLRM-GNG- 225
 : : :: | : : : | : ||:: : |
Db 166 HTLV - MKDKVASLFKKDAVLFTVDQYQEKNVDDQAGSVLLHLLEVGRVWLQYVGDD 223

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OY      226  --ALHGDHQRFSTFAGFLF 243
          | : | : ||| |||||
Db      224  HNGLYADNVNDSTFTGFLF 243

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RESULT 12
US-09-758-055-2
Sequence 2, Application US/09758055
; Patent No. US20020058617A1
; GENERAL INFORMATION:

APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard

FILE REFERENCE: 76-054-REG
CURRENT APPLICATION NUMBER: 05/09/758,055
CURRENT FILING DATE: 2001-01-10

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; TYPE: PRT
; ORGANISM: mus musculus
US-09-758-055-2

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RESULT 14
US-09-992-598--47
: Sequence 47: Application US/09992598
: Patent No. US20020160384A1
:
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
:
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C20
: CURRENT APPLICATION NUMBER: US/09/992,598
:
: CURRENT FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 60/087607
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087609
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: PRIOR APPLICATION NUMBER: 60/087759
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087827
: PRIOR FILING DATE: 1998-06-03
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: PRIOR APPLICATION NUMBER: 60/088025
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: PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/088030
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090349

PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090694
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PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 21.3%; Score 290.5; DB 9; Length 259;
Best local Similarity 28.8%; Pred. No. 3.3e-18;
Matches 78; Conservative 34; Mismatches 96; Indels 63; Gaps 10;

9 WQALLPFLPFCLODEYMSPTGGLPPCSCKC-----HGDYS 48
10 WAALLPFL---MCEIRMVELTFDRAVASGQRCDCSEDPIDPAHVSSASSSGRPALPE 66
49 FRGY-----QGPFGPGPGIPGHNNGNNGATGHEGAKGEGKGDGLGPRGERQHG 102
67 IRPYINTILKGDGKDGDPGRLGCMKREBPQGPFGQSGKD----- 109
103 PKSEKYPGIGLPELQIAFMA-----SLATHFSNONSIIIFSVETNIGNPFVYWGFGA 157
110 -KSEMGSPGAP--COKRFFAFSVGRKTAHSGEDFQTLLEFVFNLDGCGFDMATGCFMA 166

OY 158 PVSQVYFETSMKHE-DVEEYVYVLMHNGTFSMTSEMKGSDSSNNHVLTKAKD 216
Db 167 PLRGITFFSLAV--HSWYKETYVHIMNOKEAVILTA-QPSERSIMQOSVMDLAYGD 223
OY 217 EVLRLM-----NGCALHGDHOREFSTFAGFIL 242
Db 224 RWWYRLFRGRENALYSNDFYITFSGHLI 254

RESULT 15
US-09-989-293A-47
Sequence 47, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerilsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730PLC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
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PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19

Score: 1311.00 Matches: 236
 Percent Similarity: 97.15% Conservative: 3
 Best Local Similarity: 95.93% Mismatches: 7
 Query Match: 95.90% Indels: 0
 DB: 21 Gaps: 0

US-10-036-041-2 (1-246) x AAC61730 (1-1123)

QY 1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuAlaLeuPhePheLeuProPheCys 20
 Db 180 ATGCTCAGAGGAGGAGCTCGTCTGGTGGACCTGCTGCTTTCCTTCCCTCCATTTTGC 239
 QY 21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
 Db 240 CTGTGTAAATGATACATGAGATCTCCCAAGCTGGAGACTGCCCCAGACTGCAGC 299
 QY 41 LysCysGlnHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
 Db 300 AAGTGTCCCATGAGATTTGATTCCTGCTGTTACCAAGGCCCTCCGACCCAGGT 359
 QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
 Db 360 CCTCTGCGCATTCAGGAACCATGGAACAATGAAATACGAGACCACTGGCCACGAA 419
 QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyLeuArgGlyGln 100
 Db 420 GGGGCCAAGGGTGAAGAGAGACAAAGGCGCTGGGCGCTCGAGGGGAGCGGGGAG 479
 QY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
 Db 480 CATGGCCCAAGATAGAAAGGATATCCCGGGGTGCGCCAGAGCTGCAGATTGCGTTC 539
 QY 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
 Db 540 ATGGCTTCTCTACGCACTCACTTCACCAATCAGACAGTGGCATTTCTTCACACATGTT 599
 QY 141 GluThrAsnIleGlyAsnPheAspValMetThrGlyArgPheGlyAlaProValSer 160
 Db 600 GAGCCCAACATTTGGAACCTTTCATGTCATGACTGTGATTTGGGGCCCGTATCA 659
 QY 161 GlyAlaLysTyrPhePheThrPheSerMetMetLysHisGlyAspValGluGlyValTyrVal 180
 Db 660 GGGGTATTTTCTTCACCTTCACATGATGATGAGACATGAGGAGGAGGAGGATGTGTG 719
 QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys 200
 Db 720 TACCTTATGACACATGATGTAACAGCGTGTTCAGCATGTACAGTATGAAACAAAGGAAAA 779
 QY 201 SerAspThrSerSerAsnHisAlaValIleLysLysLeuAlaLysGlyAspGluValTyrLeu 220
 Db 780 TCAATATCATCCAGCAACCATGATGATGATGATGATGATGATGATGATGATGATGATG 839
 QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe 240
 Db 840 AGAATGGGCAAGCGTCCCTCCATGGGAGACACACAGCGCTTCTTACCTTCAGAGCTTT 899
 QY 241 LeuLeuPheGluThrLys 246
 Db 900 CTGCTTTTGAACACTAAG 917
 RESULT 12
 AAC99566 standard; cDNA, 1123 BP.
 AC AAC99566;
 AC 08-MAR-2001 (first entry)
 DE Skin cell cDNA, SEQ ID NO: 28.
 XX Rat; skin cell; cytostatic; anti-inflammatory; anti-HIV;
 KW neotropic; neuroprotective; vulnery; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;

KW Inflammation; neurological disease; ss.
 XX Rattus sp.
 OS WO200069884-A2.
 PN 23-NOV-2000.
 PD 15-MAY-2000; 2000WO-N200075.
 PF 14-MAY-1999; 99US-0312283.
 PR (GENE-) GENESIS RES & DEV CORP LTD.
 PA Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
 XX WPI, 2001-007495/01.
 DR P-PSDB; AAB55908.
 XX New isolated polynucleotide used in the identification of genetic
 PT disorders and encoding polypeptides used for treating inflammatory
 PT disease, cancer and neurological diseases -
 XX Claim 1; Page 87; 352pp; English.
 PS The present polynucleotide encodes a polypeptide which is expressed in
 CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
 CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.
 SQ Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other:
 XX
 Alignment Scores:
 Pred. No.: 3,366-95 Length: 1123
 Score: 1311.00 Matches: 236
 Percent Similarity: 97.15% Conservative: 3
 Best Local Similarity: 95.93% Mismatches: 7
 Query Match: 95.90% Indels: 0
 DB: 22 Gaps: 0
 US-10-036-041-2 (1-246) x AAC99566 (1-1123)
 QY 1 MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuAlaLeuPhePheLeuProPheCys 20
 Db 180 ATGCTCAGAGGAGGAGCTCGTCTGGTGGACCTGCTGCTTTCCTTCCCTCCATTTTGC 239
 QY 21 LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyLeuProProAspCysSer 40
 Db 240 CTGTGTAAATGATACATGAGATCTCCCAAGCTGGAGACTGCCCCAGACTGCAGC 299
 QY 41 LysCysGlnHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
 Db 300 AAGTGTCCCATGAGATTTGATTCCTGCTGTTACCAAGGCCCTCCGACCCAGGT 359
 QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu 80
 Db 360 CCTCTGCGCATTCAGGAACCATGGAACAATGAAATACGAGACCACTGGCCACGAA 419
 QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyLeuArgGlyGln 100
 Db 420 GGGGCCAAGGGTGAAGAGAGACAAAGGCGCTGGGCGCTCGAGGGGAGCGGGGAG 479
 QY 101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
 Db 480 CATGGCCCAAGATAGAAAGGATATCCCGGGGTGCGCCAGAGCTGCAGATTGCGTTC 539
 QY 121 MetaLaserLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140

Alignment Scores:

Pred. No.:	1,21e-117	Length:	1123
Score:	1,311.00	Matches:	236
Percent Similarity:	97.15%	Conservative:	3
Best Local Similarity:	95.93%	Mismatches:	7
Query Match:	95.90%	Indels:	0
DB:	3	Gaps:	0
US-10-036-041-2 (1-246) x US-09-188-930-203 (1-1123)			
QY 1 MetLeuTPtArgGlnLeuLeuIeYrTrpGlnLeuLeuAlaLeuPheLeuProPheCys	20		
DB 180 ARGCGACAGAGCAGCACTCGTCTGTGGCAGCACTGGCTTGCTTTGCTTCCCATTTTGGC	239		
QY 21 LeuCySGlnAspGluTrpMetClnuSerProGlnTrpGlyLeuProProAspCysSer	40		
DB 240 CMTGTGCAAGATGAATGATGAGTCTCCACAAGCTGGAGACATGCCCCCGACTGTGCAGC	299		
QY 41 LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly	60		
DB 300 AAGGTGTGCATGAGGATTTATGATTTCCGTGCTTACCAAGGGCCCCCTGGACCCCAAGT	359		
QY 61 ProProGlyIleProGlyAsnHisGlyAsnAsnGlnAsnAsnGlyAlaThrGlyHisGlu	80		
DB 360 CCTCGTGGGATTCAGGAACCATGTGAACATGAAATTAACGGAGCCACTGGCCACAGAA	419		
QY 81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln	100		
DB 420 GGGGCCAAGGGTGAAGAAAGAGACAAAGGCACTGGGGGCTCCGAGGGGAGACGGGGGAG	479		
QY 101 HisGlyProLysGlyGluLysGlyLysTrpProGlyIleProProGlyLeuGlnIleAlaPhe	120		
DB 480 CATGGCCCCAAAGAGTAGAAGGATGCCAGGGTGGCCACGAGCTGCACATTTGCCATTC	539		
QY 121 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal	140		
DB 540 AAGGCTTCTCTAGCCACTCCTTCAGCAATAGAACAGATGGCATTAATCTTAAGCAGTGT	599		
QY 141 GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer	160		
DB 600 GAGACCAACATGTGAACATCTCTCATGTCTCATGTAGATTTGGGCCCCCGGTATCA	659		
QY 161 GlyValLysPhePheThrPheSerMetMetLysHisGlyAspValGluGluValTyrVal	180		
DB 660 GCGGTGTATTTCTTACCTTCAGCTGTGATGAGCATGAGGACGTGGAGAGGTATATGTG	719		
QY 181 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGlnMetLysGlyLys	200		
DB 720 TACCTTATGCAAAATGATACAGCGGTGTTCAGCATGTACAGCTATGAACAAAGGAGAAA	779		
QY 201 SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTyrLeu	220		
DB 780 TCAGATACATCCAGCAACCATCATCAAGTGTGAAGTGGCCAAAGAGATGAAGTCTGGCTA	839		
QY 221 ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe	240		
DB 840 AAAAAAGGCGCAAGCGCCCTCCATGAGGACCAACGACGCTTCTTACCTTGCGAGGCTTT	899		
QY 241 LeuLeuPheGluThrLys 246			
DB 900 CTGCTTTTGAACACTAAG 917			
RESULT 3			
US-09-188-930-217			
: Sequence 217, Application US/09188930A			
: Patent No. 6150502			
: GENERAL INFORMATION:			
: APPLICANT: Watson, James D.			
: APPLICANT: Strachan, Lorna			
: APPLICANT: Sleeman, Matthew			
: APPLICANT: Onrust, Rene			
: APPLICANT: Murison, James Greg			
: TITLE OF INVENTION: Compositions Isolated From Skin Cells			
: TITLE OF INVENTION: and Methods For Their Use			